## **SEARCH REQUEST FORM**

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Requestor's	•	Serial		
Name:		Number:		
Date:	Phone:		Art Unit:	
Search Topic: Please write a detailed statement of search topic, that may have a special meaning. Give examples a copy of the sequence. You may include a cop	or relevant citations,	authors keywords,	etc., if known. For seq	ed. Define any terms uences, please attach
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Searcher: Beverly e 45 Terminal time: Elapsed time:	Search		Vendo	rs IG Suite STN Dialog
CPU time:	- Type	of Search		APS
Total time:	-	<ul><li>N.A. Seque</li><li>A.A. Seque</li></ul>	•	<ul><li>Geninfo</li><li>SDC</li></ul>
Number of Databases:		Structure Bibliograph		DARC/Questel Other CGN

\_ Bibliographic

PTO-1590 (9-90)

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## GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. So		,			SUMMARIES	
	core	* Query Match	Length	DB		ption
	4937	100.0	4937	!	AR032348	Seque
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RESULT 1
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LOCUS
DEFINITION Sequence 3 from patent US 5869065.
DEFINITION Sequence 3 from patent US 5869065.
ARCESSION AR032348
VERSION AR032348
CLICASSION AR032348
AROTOSION AR032348
AREFERENCE
UNKNOWN:
ORGANISM
UNCLOSSIDED
ORGANISM
TOTALE
High molecular weight surface propeins of non-typeable haemophilus
JOURNAL
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LOCATION/Qualifiers
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ce 14937 /organism="unknown" T 1729 a 948 c 1009 g 1251 t	atch 100.0%; Score 4937; DB 6; Length 4937; cal Similarity 100.0%; Pred. No. 0; 4937; Conservative 0; Mismatches 0; Indels 0; Gap	CAA CAA	CACCTTTTTGCAGTCTATATGCAAATATTTTAAAAAAATAGTATAAATCGCCCATATAA 1:	AATGGFATAATCTTTCATCTTTCATCTTTAATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCAT 11	CTTTGATCTTTCATCTTTCATCTTTCATCTTTCATCTTTGATCTTTCATCTTTCATCTTT 2.	CACATCAAATGATGAACCGAGGGAAGGGAGGGCGAAGAATGAAGAGGGGGGGCTGAAC 3(	GAACGCAAATGATAAAGTAATTTAATTGTCAACTAACCTTAGGAGAAAATATGAACAAG 30 	ATATATCGTCTCAAATTCAGCAAACGCCTGAATGCTTTGGTTGCTGTGTCTGAATTGGCA 43 	CGGGGTTGTGACCATTCCACAGAAAAGGCTTCCGCTATGTTACTATCTTTAGGTGTAAC 48 	CACTTAGCGTTAAAGCCACTTTCCGCTATGTTACTATCTTTAGGTGTAACATCTATTCA 54	CAATCTGTTTTAGCAAGCGGCTTACAAGGAATGGATGTAGTACACGGCACAGCCACTATG 60	CAAGTAGATGGTAATAAAACCATTATCGGAACAGTGTTGACGGTATCATTAATTGGAAA 66 	PACATCGACCAAAATGAAATGCTGCAGTTTTTACAAGAAAACAACAACTCCGCC 7 	GTATTCAACCGTGTTACATCTAACCAAATCTCCCAATTAAAAGGGATTTTAGATTCTAAC 78 	GGACAAGTCTTTTTAATCAACCCAAATGGTATCACAATAGGTAAAGACGCAATTATTAAC 84 	ACTAATGGCTTTACGGCTTCTACGCTAGACATTTCTAACGAAAACATCAAGGCGCGTAAT 90 	TTCACCTTCGAGCAAACCAAAGATAAAGCGCTCGCTGAAATTGTGAATCACGGTTTAATT 96 	
sourc E COUNT GIN	ery M st Lo tches	т т	61	121	181	241	301	361	421	481	541	601	661	721	781	841	901	
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AAAGACGGC 	3GTGG	CAACCATTA(           CAACCATTA(	TTGCCAAAGGC                TTGCCAAAGGC	CTGCTGATTC 	GAAGCGGAAA7 	FGATTACAGO 	8 – 8	TTAGCAAAGE 	GCGGACGCC              GCGGACGCC	GTAGTGGTC             GTAGTGGTC	TGACAG        TGACAG	FGAAGCC          FGAAGCC	SGTGAAC             GTGAAC	TATTTCAAA!             TATTTCAAA!	CGTTAATA              CGTTAATA	25 – 55 – 55	TTATTCTG	TATTA
GTCGGT        GTCGGT	TAGCGTAAATC             TAGCGTAAATC	AATAAACC          AATAAACC	CGATATTT             CGATATTT	TAAACTTT         TAAACTTT	GGGT 	CAAGCTGATC	NGGTAAAGAAGO 	CATTCAATI              CATTCAATI	SAAAAAG             SAAAAAG	SCTCAAG            SCTCAAG	TTATCCAT	GTAACAAT	AACAGGCACCC                 AACAGGCACCC	CAATACAACT/ 	GAAAACTTACO	AAAGGTCA               AAAGGTCA	TTAACCAT           TTAACCAT	TTTTTAA
1 ACT	AT	AT AT	8 – 8	8 <del>-</del> 8	AAAGA               AAAGA	8 – 8	TCAC	8 – 8	AAA 	AACC	TAT  -  TAT	GAT	0 - C - C - C	ACC ACC	AGA       AGA	AGT       AGT	AAT	GGT
961	1021	1081	1141	1201	1261	1321	1381	1441	1501	1561	1621	1681	1741	1801	1861	1921	1981	2041
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IIIIIIIII	CAAATGCTAAAATTGTCGCCCAGGCCACTGTAACCATTACAGGAGGGAAAA 2160 	GGGCTAACAACGTATCTTTAAACGGAACGGTAA 	ATAATTTAACCCACAATCTTAGTGGCACAA 	aaactacgagaaagaacacctcgtattggcaaaccagcat 	GTGCTCTTAATCTAGAGACAGGCGCAAATTTTACCTTT 	GCAAAGGCTTAACAACACAG 	GCAACATGTCATTCAATCTCAAAGAAGGAG 	AGAACATGAACACAAACCTTTACCAATTGGT 	GTGGGGGCTCTGTTTTTTTGATATATATGCCAACCATCTGGCAGAGGGGCT 2640 	AAATGAGTGAAATTAATATCTCTAACGGGGGTAATTTTACCTTAAATTCCCAT 270 	GCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACAATTCA 276 	AGCCTCAGACAGACGAAAGATGATTTTATGACGGGTACGCACGC	CCTACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCA 288 	AGCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCC 2940 	GCCCCTAATCAGCAAAACATAAGGGATAGTTATAAAACTTGGCAGCTTGCTC 3000 	GGGAGTTTAAGTTTAACTGGGGAAATGCAGATATTAAAGGCAATCTCACTATT 3060 	AGCGCCACTTT                   AGCGCCACTTT	AATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTT 3180
AAA	AAA 	299	GTGAATAA           GTGAATAA	TAACCAAAC           TAACCAAAC	16C	0-0	CAA – CAA	GAA 	7GG 1-1	AAT  -  AAT	5 – 5	8=8	5-5	25  5 		GGA GGA	929	ATG
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CAATGTT CATCATC	TGATGCT        TGATGCT	TTCCGAT           TTCCGAT	CTCTAGT             CTCTAGT	GACAGAA          GACAGAA	AGATTTA            AGATTTA	TTTTAAC             TTTTAAC	CAAAGTG	CTTAACT	AAATATC 	TGGCAAA 	GGTAAGT              GGTAAGT	AATCGGGT 	raatacggta 	ATGCGACA 	GTTCTAGG             GTTCTAGG	CAGGAAGO 	CAGGCTCC            CAGGCTCC
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CACAAGGA ACGCTAAA 1111111 ACGCTAAA	TAAATAT         TAAATAT	AAGAAGG 	AAAAGGG         AAAAGGG	TTAAAAC TTAAAAC	AGATTAC              AGATTAC	GTGCCGA              GTGCCGA	SGTCACAA              GTCACAA	AGCAATAG            AGCAATAG	SATATTAC             SATATTAC	GCTCGAC HILLIII GCTCGAC	AGCGGTAC 	rccgcrc IIIIIII	ATTGGCGC 	GTTGGGA           GTTGGGA	AATACCTC             AATACCTC	TTGGCTC.           TTGGCTC.	ACAGGCA(              ACAGGCA(
121 ACCAATAATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTT 3: 181 ACCAATGATGATGATTTAAACATTACCACTCACGCTAAACGCAACAAAGAAGGATCATC 3: 111111111111111111111111111111111111	NGGAAGCT             NGGAAGCT	TCGCAAA TCGCAAA	AACAATCA            AACAATCA	CTAACTP 	TAAAGCAG                   TAAAGCAG	TAACAGCO            TAACAGCO	TGCTGACC	ACGTGAA!             ACGTGAA!	AAACAAA(          AAACAAA(	CACAGCA(	TGATATC              TGATATC	CACTAAA	AGGTACA                AGGTACA	TTTAACA 	AACAGGG	TAGACCTC	FAAATACT           FAAATACT
CCGAAATT TAAACATT 	ACAAAAAA              ACAAAAAA	GCAATATC             GCAATATC	AACAGAT!            AACAGAT!	ATGCCAAC             ATGCCAAC	GTTTCAA'           GTTTCAA'	ATGACGG            ATGACGG	AAATCTC               AAATCTC	ATGGCGG 	TAGAAGT          TAGAAGT	TTACCAC	AAACAGG	SATTTAAC 	AGTGCAAC             AGTGCAAC	SCTGGCGA 	TTAACCGC 	GGTCAGG1            GTCAGG1	GTGACATI            GTGACATI
GGCACTGGGGTGATT	ATAATCA           ATAATCA	ATTGGCG             ATTGGCG	ATCACCA              ATCACCA	ACAAGTA 	ATTTCAG	AACAGTA	GATTCAA 	FAGCAGCA 	AAAAATG            AAAAATG	SGAAAAGG             SGAAAAGG	racaacca 	SACTGGTC             SACTGGTC	TGTAACAA                   TGTAACAA	GGCAAACO           GGCAAACO	TGCAACC	AACTAAGO             AACTAAGO	TGCTAAT
CAATAATGC CAATGATGC 	CGGAGAT	AATCCAA 	AATTAAT 	AGATGCG	ACCTAAGT	CTATTGGC 	ATGTTAA? 	AAACATCI            AAACATCI	TTACTGCA            TTACTGCA	CCGCGTCC	CAAGTAT"             CAAGTAT"	TTAGCGC         TTAGCGC	AGGCTAA'             AGGCTAA'	ATGTTAC           ATGTTAC	AAGGAGC 	TCACTTC	TTAATGC          TTAATGC
3121 ACC 3181 ACC 3181 ACC	3241 GG 11 3241 GG	3301 GA       3301 GA	3361 AA 	3421 TC     1   3421 TC	3481 GZ 1   3481 GZ	3541 AC 	3601 A2 1 3601 A2	3661 AV	3721 A	3781 A	3841 G	3901 G   3901 G	3961 G 1 3961 G	4021 A 1 4021 A	4081 G 4081 G	4141 A 4141 A	4201 A
Db Qy Db	Qy Db	Oy Dp	Qy Dp	Qy	Oy Op	Qy	Qy	Qy Db	Qy Dp	Qy Dp	Qy Dp	Oy Dp	Oy Db	Qy	Oy Db	Qy Db	Qy

Oy 4261	GATATTAAAGCAACCAGCGCACCTTGGTTATTAACGCAAAAGATGCTAAGCTAAATGGT 432	Ογ	1 TAAATATACAAGATAATAAAAATAAA
4 4		qa	1 TAAATATACAAGATAATAAAATAAA
QY 4321 Db 4321	GATCCATCAGGTGATAGTACAGAAGTGAATGCAGTCAACGCAAGCGGCTCTGGTAGTGTG 4380 	Qy Dp	61 CACCTTTTTGCAGTCTATATGCAAA 
Oy 4381 Db 4381	. ACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGTTA 4440 	ογ	
Oy 4441 Db 4441	AATATCATTTCGAAAGATGGTAGAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGGTG 450 	\ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \ \	
Oy 4501 Db 4501	AAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAACGGAAACGCGTCCTT 4	ž ov	
Qy 4561 Db 4561	GAAAAAGTAAAAGATTTATCTGATGAAGAAGAGAAACATTAGCTAAACTTGGTGTAAGT 4 	Oy Ob	
Qy 4621 Db 4621		Qy	
Qy 4681 Db 4681	ACCAGACCGTCAAGTCAAGTGATATTTCTGAAGGTGAAGCGTGTTTCTCAAGTGGTAAT 4740 	Qy	421 CGGGTTGTGACCATTCCACAGAAAAA 
Qy 4741 Db 4741		QV	
Qy 4801 Db 4801		Qy Db	
Qy 4861 Db 4861	GTTCAGTACGGGCTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTTTT 4920 	QY Db	601 CAAGTAGATGGTAATAAAACCATTATC 
Qy 4921 Db 4921	AACAGGTTATTATTATG 4937 	Qy	
RESULT 2 AR083955 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	AR083955	Qy Db Qy	721 GTATTCAACCGTGTTACATCTAACCAA.
SOURCE ORGANISM REFERENCE		Qy. Db	841 ACTAATGGCTTTACGGCTTCTACGCTAC 
AUTHORS TITLE JOURNAL FEATURES	Barenkamp, S.J. High molecular weight surface proteins of non-typeable haemophilus Patent: US 597736-A 3 02-NOV-1999; Location/Qualifiers	Qy	901 TTCACCTTCGAGCAAACCAAAGATAAAC 
source BASE COUNT ORIGIN		Qy	961 ACTGTCGGTAAAGACGGCAGTGTAAATC 
Ouery Ma Best Loo Matches	Ouery Match 100.0%; Score 4937; DB 6; Length 4937; Best Local Similarity 100.0%; Pred. No. 0; Matches 4937; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy	1021 ATTAGGSTAAATGSTGGCAGCATTTCTT 

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CTTTAATCTTTCATCTTTCATCTTTCATTTCAT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATATTTTAAAAAAAATAGTATAAATCCGCCATATAA 120
                                                             ATCTTTCATCTTTCATCTTTCATCTTTCATCTTT 240
                                                                                                                                                            TGTTCAACTAACCTTAGGAGAAATATGAACAAG 360
                                                                                                                                                                                                                                                                                                           TTACTCGCAGGCAAAAATCACCATCAGCGAT 1080
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                                                                                                                                                                                                                                                                                               CCTGAATGCTTTGGTTGCTGTCTGAATTGGCA 420
                                                                                                                                                                                                                                                                                                                                              AGGCTTCCGCTATGTTACTATCTTTAGGTGTAAC 480
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              AGGAATGGATGTACACGGCACAGCCACTATG 600
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ATCAAGATTTTTGTGATGACAACAACAATTACAA 60
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Q dq	2221	CAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACA 228 
y 0 4	28	AACCAAACTACGAGAAAGAACACCTCGTATTGGCAAACCAGCCATGATTCGCACTGG 23
oy i	1 8	CAGTGCTCTTAATCTAGAGACAGGCGCAAATTTACCTTATTATAAATACATTCA 240
oy Oy	2341	CGTCAGTGCTCTTAATCTAGAGACAGGCGCAAATTTTACCTTTATAAATACATTTCA 240 CAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGC 246
: a	40	GCAGGGGTGAATTTTAACGGC 246
ò d	2461	AATGGCAACATGTCATTCAATGTCAAAGAAGGAGCGAAAGTTAATTTCAAATTAAAA 255 8 ATGC SACATGT
δŏ	52	CAAACGAGAACATGAACAAGCAAACCTTACCAATTCGGTTTTAGCCAATATCACA 258
qq	52	ACGAGAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACA 258
Qy Dp	2581	CAACCATTCTGGCAGAGGGGT 264
Qy	4	TAAAAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCCCAT 270
Dp	2641	agitaaaaatgagtgaaattaatatctctaacggcgctaattttaccttaaattcccat 2
QY	2701	5GGGGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCA 
Οy	2761	TTCAGCCTCAGACGAAGAAGATGATTTTTATGACGGGTACGCAAGCAA
QQ	2761	TTATGACGGGTACGCACGCAATGCCATC 2
ον.	82	TCAACCTACAACATATCCATTCTGGGGGGTAATGTCACCCTTGGTGGACAAAACTCA 2
g À	2821	ICAACCIACAACAIAICCAIIICIGGGGGIAAIGICACCCIIIGGIGGAGAAAACICA Z GGCAGCAIIACGGGGAAAAIIACIAICGAGAAAGCAGCAAAIGIIAGGGIAGAAAGC Z
g qq	88	SAAAGCAGCAAATGTTACGCTAGAAGCC 2
QY	2941	AACGCCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC 3
Ωp	4	CCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC 3
ογ	00	AAATGGGAGTTTAAGTTTAACTGGGGAAAATGCAGATATAAAGGCAATCTCACTATT 306
2 0	3061	IAATGGGAGITTAAGITTAACITTAACIGGGGAAAANIGGGAGTATTAAAAGGGGGAGTTTAAAAAAAGGGGGAATTTT
g qq	90	
οy	3121	CAATAATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTT 318
Db	3121	CCAATAATGGCACTGCCGAAATTAATATAACACAGAGTGGTGGTAAACTTGGCAATGTT 318
Q 4	3181	CAATGATGATGATTAAACATTACCACTCACGCTAAACGAACCAAAGAAGAATTAATC 3 CAATGATTAAAACATTACCACTCACGCTAAAACGAACCAAAAGAAGAATTAATT
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3241	. GGCGGAGATATAATCAACAAAAAAGGAAGCTTAAATATTACAGACAG	
3301	GAAATCCAAATTGGCGGCAATAFCTCGCAAAAAGAAGGCAACCTCACGATTCTTCCGAT 3360 	
3361 3361	AAAATTAATATCACCAAACAGATAACAATCAAAAGGGTATTGATGGAGGGGGCTCTAGT 3420 	
3421	TCAGATGCGACAAGTAATGCCAACCTAACTATTAAAACCAAAGAATTGAAATTGACAGAA 3480 	
3481	GACCTAAGTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTA 3540 	
3541	ACTATTGGCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTAAC 3600 	
3601	AATGTTAAAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTG 3660 	
3661	AAAACATCTAGCAGCAATGGCGGACGTGAAAGCAATAGCGACAACGATACCGGCTTAACT 3720 	
3721 3721	ATTACTGCAAAAATGTAGAAGTAAACAAAGATATTACTTCTCTGAAACAGTAAATATC 3780 	
3781 3781	ACCGCGTCGGAAAAGGTTACCACCACAGGGTCGACCATTAACGCAACAATGGCAAA 3840 	
3841	GCAAGTATTACAACCAAAACAGGTGATATCAGCGGTACGATTTCCGGTAACACGGTAAGT 3900 	
3901 3901	GTTAGCGCGACTGGTGATTTAACCACTAAATCCGGCTCAAAAATTGAAGCGAAATCGGGT 3960 	
3961 3961	GAGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGGTA 4020 	
4021	AATGTTACGGCAAACGCTGGCGATTTAACAGTTGGGAATGGCGCAGAATTAATGCGCA 4080 	
4081	GAAGGACCTGCAACCTTAACCGCAACAGGAATACCTTGACTACTGAAGCCGGTTCTAGC 4140 	
4141	ATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAAGC 4200	
4201	ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACGTGGCAGGCTCG 4260 	
4261	GATATTAAAGCAACCAGGGACCTTGGTTATTAACGCAAAAGATGCTAAGCTAAATGGT 4320 	
4321	GATGCATCAGGTGATAGTACAGAAAGTGAATGCAGCGAGCG	

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Barenkamp,S.J.
High molecular weight surface proteins of non-typeable haemophilus
Patent: US 6218141-A 3 17-APR-2001;
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Qy Dp	2341	1 AACGTCAGTGCTCTTAATCTAGAGACAGGCGCAAATTTTACCTTTATTAAATACATTTCA	2400
Qy Dp	2401	AGCAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGTGAATTTTAACGG 	46
Qy Dp	2461	GTAAATGGCAACATGTCATTCAATCTCAAAGAAGGAGCGAAAGTTAATTTCAATTAAA. 	522
QY	2521	CCAAACGAGAACATGAACACAAGCAACCTTTACCAATTCGGTTTTTAGCCAATATCAC 	58
Qy Db	2581	GCCACTGGTGGGGGCTCTGTTTTTTGATATATGCCAACCATTCTGGCAGGGGCT 	64
Qy	2641	GAGTTAAAAATGAGTGAAATTAATATCTCTAACGGGGCTAATTTYACCTTAAATTCCAT 	2700
Qy Db	2701	GTTCGCGGCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAACGAACCAATTCA	2760
Qy Db	2761 2761	AATTTCAGCCTCAGACAAAGATGATTTTTATGACGGGTACGCACGC	2820
Oy Dp	2821	AATTCAACCTACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCA ;	2880
Qy	2881	ACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCC	2940
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25 25	3001	GTTAATGGGAGTTTAAGTTTAACTGGGGAAAATGCAGATATTAAAGGCAATCTCACTATT 3	3060
Oy Db	3061 3061	TCAGAAAGCGCCACTITTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATITT 3 	3120
Qy Db	3121	AGTGGTAAAACTTGGCAATGTT 	3180
Qy Db	3181	ACCAATGATGGTGATTTAAACATTACCACTCACGCTAAACGCAACCAAGGAGGATCATC 3	24
oy Op	3241 3241	GGCGGAGATATAATCAACAAAAAGGAAGCTTAAATATTACAGACAG	300
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                                                                                                          GGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACAAG 4800
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4501 AAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCCTT 4560
           1561 GAAAAAGTAAAAAGATTAATCTGATGAAGAAAGAGAAACATTAGCTAAAACTTGGTGTAAGT 4620
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               301 GAACGCAAATGATAAAGTAATTTAATTGTTCAACTAACCTTAGGAGAAAATATGAACAAG 360
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2401 AGCAATAGCAAAGGCTTAACAACAACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGC 2460 2640 2640 2700 2700 2760 2760 2820 2820 2880 2940 2940 3000 3060 3060 3120 3120 3180 2941 AATAACGCCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC 3000 3180 3240 3240 3300 3360 3300 3360 3420 TCAGATGCGACAAGTAATGCCAACCTAACTATTAAAACCAAAGAATTGAAATTGACAGAA 3480 GACCTAAGTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTA 3540 CCAAACGAGAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACA 2641 GAGTTAAAAATGAGTGAAATTAATATCTCTAACGCGCCTAATTTTACCTTAAATTCCCAT GAGTTAAAAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCCCAT 2821 AATTCAACCTACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCA 2581 GCCACTGGTGGGGGCTCTGTTTTTTTGATATATGCCAACCATTCTGGCAGAGGGGCT GTTCGCGGCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCA 2881 AGCAGCAGCATTACGGGGAATATTACTATCGAGAAAAGCAGCAAATGTTACGCTAGAAAGCC AGCAGCAGCATTACGGGGAATATTACTATCGAGAAAGCAGCAAAATGTTACGCTAGAAGCC 3001 GITAATGGGAGTITAAGIITAACIGGGGAAAATGCAGATAITAAAGGCAAICICACIAIT 3061 TCAGAAAGCGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTTT GAAATCCAAATTGGCGGCAATATCTCGCAAAAAGAAGGCAACCTCACGATTTCTTCCGAT GTTAATGGGAGTTTAAGTTTAACTGGGGAAAATGCAGATATTAAAGGCAATCTCACTATT ACCAATAATGGCACTGCCGAAATTAATAAACACAAGGAGTGGTAAAAACTTGGCAATGTT AAAATTAATATCACCAAACAGATAACAATCAAAAAGGGTATTGATGGAGAGGACTCTAGT 2521 2641 2701 2701 2761 2821 2941 2521 2881 3001 3121 3301 3481 3361 3361 3421 ò d ò Ω ò g δy Db ò g ò g Qγ Ω δy QQ ò g QQ οy Ω pp ò qq Óγ g Ω δý à . q ò q ò QQ ò

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Barenkamp.S.J.
High molecular weight surface proteins of non-typeable haemophilus Patent: US 5603938-A 3 18 FEB-1997;
Location/Qualifiers
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GCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTTACA 4680
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1441 GGCATTCAATTAGCAAAGAAAACCTCTTTAGAAAAGGCTCAACCATCAATGTATCAGGC 1500 1680 1681 GATGTAACAATTGAAGCCGAAGACCCCTTCGCAATAATACCGGTATAAATGATGAATTC 1740 1740 1800 1860 1920 1920 1980 1980 2040 2040 1680 1860 2100 2100 2160 2220 2280 2460 AACGTCAGIGCTCTTAATCTAGAGACAGGGGGAAATTTTACCTTTATAAATACATTTCA 2400 2461 GTAAATGGCAACATGTCATTCAATCTCAAAGAAGGAGCGAAAGTTAATTTCAAATTAAAA 2520 CCAAACGAGAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACA 2580 1501 AAAGAAAAAGGCGGACGCGCTATTGTGTGGGGGCGATATTGCGTTAATTGACGCCAATATT AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGGAGACATCGGGGCAT TATTTATCCATTGACAGCAATGCAATTGTTAAAACAAAAGAGTGGTTGCTAGACCCTGAT 1861 AGAAAACTTACCGTTAATAGCTCAATCAACATGGGAAGCAACTCCCACTTAATTCTCCAT 1861 AGAAAACTTACCGTTAATAGCTCAATCAACATCGGAAGCAACCACTTAATTCTCCAT 1921 AGTAAAGGTCAGCGTGGCGGAGGCGTTCAGATTGATGGAGATATTACTTCTAAAGGCGGA AATTTAACCATTTATTCTGGCGGATGGTTGATGTTCATAAAATATTACGCTTGATCAG 1981 ATTTAACCATTATTCTGGGGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG 2041 GGTTTTTAAATATACGGCGGCTTCGGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 1041 GGTTTTTTAAATATTACGGCGCTTCCGTAGCTTTTGAAGGTGGAATAACAAGCACGC GACGCGCCAAATGCTAAAATTGTCGCCCAGGGCACTGTAACCATTACAGGAGAGAAAA TCAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACA CCAACAGGCACCGGTGAAGCAAGCGACCCTAAAAAAATAGCGAACTCAAAACAACGCTA **ACCAATACAACTATTTCAAATTATCTGAAAAACGCCTGGACAATGAATATAAACGGCATCA** GATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 2461 GTAAATGGCAACATGTCATTCAATGTCAAAGAAGGAGGAAAGTTAATTTCAAATTAAAA AGCAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGC 1621 1681 1741 1561 1621 1801 1981 2101 2101 2161 2161 2221 2401 2401 2281 2281 2221 2341 2341 2521 δ g QQ ò οp Db δŽ ò Op ò g QQ δ ò g ò qq Dp Qγ ΩD Ω ŏ Ω ò qq δý οq οy q ò Ωp ò Op ά

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	AATTTCAGCCTCAGACGAAAGATGATTTTATGACGGGTACGCACTAGTCATTTCAGCCTCAATTCAGCGGGTACGCAATGCCAATTCAGCGCTAATTTTTATGACGGGTACGCAATGCCAATTGCCATTGTTTTTTTT	TCAGAAAGCGCCACTTTAAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAAT	GAAATCCAAATTGGCGGCAATATCTCGCAAAAGAGGCAACCTCACGATTCTTCCGAT   IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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4801 GTAGATTTCATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTACTGTGTGGGGTTAAA 4860
                                                          GITCAGTACGGGCTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTTT 4920
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                                     361 ATATATCGTCTCAAAATTCAGCAAACGCCTGAATGCTTTGGTTGCTGTGTCTGAATTGGCA 420
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y do	1441	GGCATTCAATTAGCAAAGAAAACTCTTTAGAAAAAGGCTCAACCATCAATGTATCAGGC 1 	1500
Qy Db	1501	AAAGAAAAAGGGGACGCGCTATTGTGTGGGGCGATATTGCGTTAATTGACGGCAATATT	1560 1560
oy Op	1561	AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGGAGACATCGGGGCAT	1620 1620
Oy Dp	1621 1621	ACAAAAGAGTGGTTGCTAGACCCTGAT 	1680
Qy Db	1681	GATGTAACAATTGAAGCCGAAGACCCCTTCGCAATAATACCGGTATAAATGATGAATTC :	1740
Qy Db	1741	CCAACAGGCACGGGGAAGCAACGACCCTAAAAAAATAGGGAACTCAAAACAAGGTG :	1800
Oy Dp	1801	ACCAATACAACTATTTCAAATTATCTGAAAAACGCCTGGACAATGAATATAACGGCATCA	1860
Q Dp	1861 1861	AGAAAACTTACCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCGACTTAATTCTCCAT	1920 1920
Oy Dp	1921	AGTAAAGGTCAGCGTGGCGGAGCGTTCAGATTGATGGAGATATTACTTCTAAAGGCGGA 	1980 1980
oy Op	1981	AATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG 	2040
Oy Dp	2041	GGTTTTTTAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 	2100
Qy	2101	GACGCGCGAAATGCTAAAATTGTCGCCCAGGCACTGTAACCATTACAGGAGAGGAAAA 	2160
Oy Db	·2161 2161	GATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 	2220
Oy Db	2221	CACAATTAACATA 	
Qy Db	2281	AAAGAACACCTCGTATT( 	2340
Qy Db	2341	AACGTCAGTGCTCTTAATCTAGAGACAGGCGCAAATTTTACCTTTATTAAATACATTTCA	2400
QY Db	2401	AGCAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGC 	2460

3600	3660	3720	3780	384	390	396 396	4020	4080	4140	4200	4260	4320	4380	4440	4500	4560	4620	4680
	AATGTTAAAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTG	AAAACATCTAGCAGCAATGGCGGACGTGAAAGCAATAGCGACACGATACCGGCTTAACT	ATTACTGCAAAAATGTAGAAGTAAAAGAAGATATTACTTCTCTCAAAACAGTAAATAC 	ACCGCGTCGGAAAAGGTTACCACACAGAGGCTCGACCATTAACGCAACAAAATGGCAAAAAAACCGAAAAAAAGCAAAAAAAGGCAAAAAAAGCAAAAAA	STACGATTTCCGGTAACACG 	GTTAGCGCGACTGGTGATTTAACCACTAAATCCGGCTCAAAAATTGAAGCGAAATCGGGT 	GAGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGGTA 	AATGTTACGGCAAACGCTGGCGATTTAACAGTTGGGAATGGCGCAGAAATTAATGCGACA 	GAAGGAGCTGCAACCTTAACCGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCTAGC	ATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAAGC	ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACGGTGGCAGGCTCG	GATATTAAAGCAACCAGCGGCACCTTGGTTATTAACGCAAAAGATGCTAAGCTAAATGGT 	GATGCATCAGGTGATAGTACAGAAGTGAATGCAGCGACGCGGGCTCTGGTAGTGTG 	ACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGTTA 	AATATCATTTCGAAAGATGGTAGAAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGGTG	AAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCCTT 	GAAAAAGTAAAAGATTTATCTGATGAAGAAAGAGAAACATTAGCTAAACTTGGTGTAAGT 	GCTGTACGTTTTGTTGAGCCAAATACAATTACAGTCAATACACAAAATGAATTTACA
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Submitted (14-APR-1994) Stephen J. Barenkamp, Department of Submitted (14-APR-1994) Stephen J. Barenkamp, Department of Pediatrics, St. Louis University School of Medicine, Cardinal Glennon Children's Hospital, 1465 South Grand Boulevard, St. Louis, MO 63104-1095, USA
On May 5, 1994 this sequence version replaced gi:148904.

Location/Qualifiers
1. 18983
//Organism="Haemophilus influenzae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear BCT 05-AUG-1994
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8983 bp DNA linear BCT 05-AUG-1994
Haemophilus influenzae strain 12 adhesin (hmw2A) gene and putative
accessory processing proteins (hmw2B) and (hmw2C) genes, complete
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Barenkamp, S.J. and Leininger, E.
Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Haemophilus influenzae high-molecular-weight surface-exposed proteins related to filamentous hemagglutinin of Bordetella pertussis
                                      4681 ACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTAAT 4740
                                                         4621 GCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTTACA 4680
                                                                                                            4741 GCCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACAAG 4800
                                                                                                                                 /clone_lib="Lambda EMBL3 genomic library of strain 12" 130. 241 /citation=[1]
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Haemophilus influenzae
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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Barenkamp, S.J. and St Geme, J.W. III.
Genes encoding high-molecular-weight adhesion proteins of nontypeable Haemophilus influenzae are part of gene clusters Infect. Immun. 62 (8), 3320-3328 (1994)
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352. .4785
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Barenkamp, S.J.
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VEHIDEGLEKRLGLPPWLADTRETYIECALRLAENHQERLELRRYIIENNGLOKLF
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                                                           99.3%; Score 4900.2; DB 1; Length 9983; 99.5%; Pred. No. 0;
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ATTGGTGGCAA/ ATTGGTGGCAA/ ATTGTGGTGCAA/ ATTGTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	1141 GCGGATATTTTGCCAAAGGCGGTAACATTAATGTCCGTGGT	1321 GGCAAGCTGATACCGGAATTGGCGGTGTAATTTCCGGTC 1321 GGCAAGCTGATGATTACAGCGGTTAAAAA 1321 GGCAAGCTGATGATTACAGCGGATAAAGTCACATTAAAAA 1381 TCAGGTAAAGAGGGGAGAAACTTACTTGCGGTGACG 1381 TCAGGTAAAGAAGGGGAGAAACTTACTTGCGGGTGACG	1441 GGCATTCAATTAGCAAAGAAAACCTCTTTAGAAAAAGGCTCA 	1561 AACGCTCAAGGTAGTGATATCGCTAAAACGGGTGGTTT 1561 AACGCTCAAGGTGGTGGTGTTTTTTTTTTTTTTTTTTTT	1741 CCAACAGGCACCGGTGAAGCAAGCGACCCTAAAAAAATAGC	1921 AGTAAAGGTCACCGGAGGCGTTCAGATGATGAGGAGTACAGAGGTACAGAGGTACAGGGTGAGGGAGG
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4201 ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACGTGGCAGGCTCG 4260
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                                                     3181 ACCAATGATGGTGATTTAAACATTACCACTCACGCTAAACGCAACCAAAGAAGCATCATC 3240
                                                                                       GAAATCCAAATTGGCGGCAATATCTCGCAAAAGAAGGCAACCTCACGATTTCTTCCGAT 3360
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Barenkamp, S.J. and St. Geme, J. William. III.

High molecular weight surface proteins of non-typeable haemophilus
Patent: US 5869065-A 6 09-FEB-1999;
Location/Qualifiers
1. 9323
                                                                                                                                                                                                4861 GTTCAGTACGGGCTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTTT 4920
                                                                                                     4621 GCTGTACGTTTTGTTGAGCCAAATAATAACAGTCAATACACAAAATGAATTTACA 4680
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                                                                                  4321 GATGCATCAGGTGATAGTACAGAAGTGAATGCAGTCAACGCAAGCGGCTCTGGTAGTGTG 4380
                                                                                                                                           4381 ACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGTTA 4440
                          4261 GATATTAAAGCAACCAGCGGCACCTTGGTTATTAACGCAAAAGATGCTAAGCTAAATGGT 4320
4201 ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGCTCG 4260
                                         Score 4820.2; DB 6; Length 9323;
Pred. No. 0;
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Sequence 6 from patent US 5869065.
AR032350 11:5947955
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Best Local Similarity
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δy	61 CACCITITITGCAGTCTATATGCAAATATTTTAAAAAATAGTATAAATCGCCATATAA 12
qq	01 CACCTTTTTTGCAGTCTATATGCAAATATTTTAAAAAAATAGTATAAATCCGCCATATAA 56
Oy Pp	121 AATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATCTTTCATCTTTCATCTTTCAT 180 
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oy da	301 GAACGCAAATGATAAAGTAATTTAATTGTCAACTAACCTTAGGAGAAAATATGAACAAG 360 
6 da	361 ATATATGGTCTCAAATTCAGCAAAGGCCTGAATGCTTTGGTTGCTGTGTCTGAATTGGCA 420 
6y 4	21 CGGGGTTGTGACCATTCCACAGAAAAGGCTTCCGCTATGTTACTATCTTTAGGTGTAAC 48
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Oy 6	601 CAAGTAGATGGTAATAAAACCATTATCGGCAACAGTGTTGACGCTATCATTAATTGGAAA 660 
Oy 6 Db 11	661 CAATTTAACATCGACCAAAATGAAATGGTGCAGTTTTTACAAGAAAACAACAACCACCCC 720 
Qy 7 Db 11	721 GTATTCAACCGTGTTACATCTAACCAAATCTCCCAATTAAAAGGGATTTTAGATTCTAAC 780 
Qy 7 Db 12	/81 GGACAAGTCTTTTAATCAACCCAAATGGTATCACAATAGGTAAAGACGCAATTATTAAC 840 
Qy 8 Db 12	841 ACTAATGGCTTTACGGCTTCTACGCTAGACATTCTAACGAAAACATCAAGGGGGGGG
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1200 1640 1260 1320 ATAATAAACCCAACCATTACTTACAGCATTGCCGCGCGTGAAAATGAAGCGGTCAATCTG 1140 1760 1380 1820 1440 1880 1500 1560 2000 1620 2060 1680 2120 1740 2180 1800 2240 1980 2360 2420 2040 2480 2100 2540 GGTAAACTTTCTGCTGATTCTGTAAGCAAAGATAAAAGCGGCAATATTGTTCTTTCCGCC AAAGAGGGTGAAAGCGGAAAATTGGCGGTGTAATTTCCGCTCAAAATCAGCAAGCTAAAGGC GGCAAGCTGATGATTACAGGCGATAAAGTCACATTAAAAACAGGTGCAGTTATCGACCTT 2001 AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGGAGACATCGGGGCAT AAAGAAAAAGGCGGACGCGTATTGTGTGGGGCGATATTGCGTTAATTGACGGCAATATT AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTTGTGGAGACATCGGGGCAT GATGTAACAATTGAAGCCGAAGACCCCCTTCGCAATAATACCGGTATAAATGATGAATTC CCAACAGGCACCGGTGAAGCAAGCGACCCTAAAAAAAATAGCGAACTCAAAACAACGCTA AGTAAAGGTCAGCGTGGCGGAGGCGTTCAGATTGATGGAGATATTACTTCTAAAAGGCGGA AATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG GGTTTTTTAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 1081 1141 1581 1641 1261 1701 1821 1441 1501 1941 1201 1321 1761 1381 1881 1561 1741 2241 1621 2061 1681 2121 1801 1861 2301 2361 1981 2421 2041 2541 1921 2481 2101 g qq ò ð g δ qq ŏ Ω g δ δ g ò qq g pp ò ò ò a à QQ g g Ω ŏ ŏ q g δý ò Op ŏ

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368	30	3361	342	348.	354	360	366	372	378	384	390	396	402	408	414	420	426	432
qq	Qy Db	Qy	Qy Db	Qy Db	QY Db	QY	QY	Qy	Qy	Qy	QY	Qy	Qy	Qy	Qy	Qy	Qy Db	Qy

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OY 4381 ACTGCGCCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGTTA 4440	OY 4441 AATATCATTTCGAAAGATGGTAGAAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGGTG 4500	Qy 4501 AAATATGCAGCCAGGTGTAGCAAGTGTAGAAGTAATTGAAGCGAAACGCGTCCTT 4560	QY 4561 GAAAAAGTAAAAGATTTATCTGATGAAGAGAAACATTAGCTAAACTTGGTGTAAGT 4620 	QY 4621 GCTGTACGTTTTGTTGAGCCAAATAATACAGTCAATACACAAAATGAATTTACA 4680 	QY       4681       ACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGCGTGTTTCTCAAGTGGTAAT 4740         DD       111111111111111111111111111111111111	QY 4741 GGCGCACGAGTATGTACCAATGTTGCTGACGATGGACGCGTAGTCAGTAATTGACAAG 4800 D1	Qy 4801 GTAGATTTCATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTACTGTGTGGGTTAAA 4860 	QY 4861 GTTCAGTACGGCCTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTTT 4920 	OY 4921 AACAGGTTATTATG 4937 	AR083957	TITLE High molecular weight surface proteins of non-typeable haemophilus JOURNAL Patent: US 5977336-A 6 02-NOV-1999; FEATURES Location/Qualifiers Source 1. 9323 /organism="unknown" BASE COUNT 3134 a 1829 c 1832 g 2528 t	Ouery Match 97.6%; Score 4820.2; DB 6; Length 9323; Best Local Similarity 98.5%; Pred. No. 0; Matches 4864; Conservative 0; Mismatches 73; Indels 0; Gaps 0;	QY 1 TAAATATACAAGATAATAAATAAATCAAGATTTTTGTGATGACAAACAA
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GGTAAACTITCTGGTGAITCIGTAAGCAAAGATAAAAGGGGGAATAITGTTCTITCGGCC 1260 	AAAGAGGGTGAAGCGGAAATTGGCGGTGTAATTTCCGCTCAAAATCAGCAAGCTAAAGGC 1320 	AAGCTGATGATTACAGGCGATAAAGTCACATTAAAAACAGGTGCAGTTATCGACCTT 138 	CAGGTAAAGAAGGGGAGAAACTTACCTTGGCGGTGACGAGGGGGGGG	CATTCAATTAGCAAAGA 	GGAAAAAGGCGGACGCCTATTGTGTGGGGCGATATTGCGTTAATTGACGGCAATATT 1	SCTCAAGGTAGTGGTG 	TPATCCATTGACAGCAATGCAATTGTTAAAACAAAAGAGTGGTTGCTAGACCCTGAT 1680 	ATGTAACAATTGAAGCCGAAGACCCCCTTCGCAATAATACCGGTATAAATGATGATGATTC 174 	CCAACAGGCACCGGTGAAGCGACCCTAAAAAAATAGCGAACTCAAAACAACGT 180 	ACCASTACAACTATTTCAAATTATCTGAAAAAGGCCTGGACAATGAATATAACGGCATCA 186	AGAAAACTTACCGTTAATAGCTCAATCAACATGGGAAGCAACTCCCACTTAATTCTCCAT 192 	AGTAAAGGTCAGCGTGGCGGAGGCGTTCAGATTGATGGAGATATTACTTCTAAAGGCGGA 196 	AATTTAACCATTTATTCTGGGGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG 20	GGTTTTTAAATATTACGCCGCTTCCGTAGCTTTGAAGGTGGAAATAACAAAGCACGC 21. 	GACGGGGCAATGCTAAAATTGTCGCCCAGGGCACTGTAACCATTACAGGAGAGGGAAAA 216	1 GATTTCAGGGCTAACAACGTATCTTAAACGGAAACGGAAATTCAGGGCTAACAACGTATCTTTAAACGGAAACGTAACAACGTATCTTTAAACGGAA	1 TCAGTGAATAATTTAACCCACAATCT 
201 GGT      641 GGT	261	321 G   	381 TC 11 821 TC	441 GG 	501	561	621	681	741	801 A 241 A	861	921	981	041	101	161	221
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                                                                         4881 AATATCATTICGAAAGAIGGIAGAAACACTGIGCGCTIAAGAGGCAAGGAAATIGAGGIG 4940
                       4501 AAATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGGAAACGCGTCCTT 4560
                                       4941 AAATATECEAGCEAGGTGTAGCAAGTGTAGAAAGTAATAGAAGGAAACGCGTCCTT 5000
                                                                                                                           4621 GCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAAATGAATTTACA 4680
                                                                                                                                         4681 ACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTAAT 4740
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Qy	1321	GGCAAGCTGATGATTACAGGCGATAAAGTCACATTAAAAACAGGTGCAGTTATCGACCTT 13 	180
δδ	1381	CAGGTAAAGAAGGGGGAGAAACTTACCTTGGCGGTGACGAGCGCGGCGAAGGTAAAAAC 14	4
qa ,	1821		æ
δλ	1441	CAACCATCAATGTATCAGGC 15	0
qq	1881	GCATTCAATTAGCAAAGAAAACTCTTTAGAAAAAGGCTCAACCATCAATGTATCAGGC 19	40
QY	0		9
DP	1941	BAAAAAGGCGGACGCCTATTCTGTGGGGCGATATTGCGTTAATTGACGGCAATATT 20	Ō
Qy	1561	CGGTGGTTTTGTGGAGACATCGGGGCAT 16	Ö
qq	2001	CCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGGAGACATCGGGGCAT 20	9
οy	1621	AAAACAAAAGAGTGGTTGCTAGACCCTGAT 16	æ
ΩD	2061	ATTTATCCATTGACAGCAATGCAATTGTTAAAACAAAAGAGTGGTTGCTAGACCCTGAT 21:	20
Οy	1681	TCGCAATAATACCGGTATAAATGATGAATTC 17	4
DP	2121	ATGTAACAATTGAAGCCGAAGACCCCTTCGCAATAATACCGGTATAAATGATGATGATTC 21	80
QY	1741	GGTGAAGCAAGCGACCCTAAAAAATAGCGAACTCAAAACAACGCTA 18	00
qq	2181	CAACAGGCACCGGTGAAGCAAGCGACCCTAAAAAAATAGCGAACTCAAAAACAACGCTA 22	40
QY	1801	CCAAATTATCTGAAAAACGCCTGGACAATGAATATAACGGCATCA 18	09
QQ	2241	AATACAACTATTTCAAATTATCTGAAAAACGCCTGGACAATGAATATAACGGCATCA 23	00
Qy	1861	CCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATTCTCCAT 19	20
qa	2301	AAAACTTACCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATTCTCCAT 23	09
Qy	1921	SCGGAGGCGTTCAGATTGATGGAGATATTACTTCTAAAGGCGGA 19	8
qq	2361	STCAGCGTGGCGGAGGCGTTCAGATTGATGGAGATATTACTTCTAAAGGCGGA 24	20
Qy	1981	TGGCGGATGGGTTGATCATAAAAATATTACGCTTGATCA	
QQ	2421	TTAACCATTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG 24	80
Qy	2041	CGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 21	00
qa	2481	rttti	40
Οy	2101	GTCGCCCAGGGCACTGTAACCATTACAGGAGGG	09
qq	2541	ACGCGCCAAATGCTAAAATTGTCGCC	00
Qy	2161	TATCTTTAAACGGAACGGGTAAAAGGTCTGAATATCATTTC	20
qq	2601	TCAGGGCTAACAA	90
QY	2221	TTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACA 228	30
QQ	2661	CAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACA 272	20
δλ	2281	CTCGTATTGGCAAACCAGCCATGATTCGCACTGG 234	0 ;
qq	2721	TTAACCAAACTACGAGAAAGAACACCTCGTATTGGCAAACCAGCCATGATTGGCACGG 278	000
QY	2341	AGTGCTCTTAATCTAGAGACAGGGGCAAATTTTACCTTTATTAAATACATTTCA 240	00
QQ	2781	CSTCAGIGCICTIAATCIAGAGACAGGGGGAAITTTACCTITATTAAAIACAITTCA 284	0

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AATATCATTTCGAAAGATGGTAGAAACACTGTGCGCTTAAGAGGCAAGGAATTGAGGTG 4500 4620 3600 3780 4280 3900 4340 3960 4400 4460 4080 4140 4200 4640 4260 3921 GACCTAAGTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGAGTTTA 3980 4760 GATGCATCAGGTGATAGTACAGAAGTGAATGCAGTCAACGCAAGCGGCTCTGGTAGTGTG 4380 ACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGGATTTAAACACAGTAAATGGGTTA 4440 AAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCCTT 5000 GAAAAAGTAAAAGATTTATCTGATGAAGAAAGAGAAACATTAGCTAAACTTGGTGTAAGT AAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCCTT ACTATTGGCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCCAAAACAGTAACTTTTAAC AATGTTAAAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTG GTTAGCGCGACTGGTGATTTAACCACTAAATCGGGCTCAAAAATTGAAGCGAAATCGGGT GAGGCTAATGTAACAACTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGGTA AATGTTACGGCAAACGCTGGCGATTTAACAGTTGGGAATGGCCCAGAAATTAATGCGACA GAAGGAGCTGCAACCTTAACCGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCTAGC ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACGTGGCAGGCTCG ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGCTCG ACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGTTA AAAACATCTAGCAGCAATGGCGGACGTGAAAGCAATAGCGACAACGATACCGGCTTAACT ACCGCGTCGGAAAAGGTTACCACACAGCAGGCTCGACCATTAACGCAACAAATGGCAAA GAGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGGTA ATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAAGC 3601 3781 3961 4401 4461 4581 4201 4321 4441 4881 4501 4941 4561 3661 4101 3901 4081 4521 4141 4641 4381 3541 4021 4821 g QQ QΩ pp qq Q δy g g ŏ qq ò g ò Dp ò g ŏ qq ò pp ò qq ò qq ò g ŏ ò ò ŏ á ò ò

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1 (bases 1 to 9323)
Barenkamp.S.J. and St. Geme,J.W. III.
High molecular weight surface proteins of non-typeable haemophilus patent: US 5549897-A 6 27-AUG-1996;
Location/Qualifiers
1. 9323 "...brown"
                                                                                                                                                                                               301 GAACGCAAATGATAAAGTAATTTAATTGTTCAACTTAAGGAGAAAATTTGAACAAG 360
                                  4741 GGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACAAG 4800
                                                                                                                                                    GTAGATTTCATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTACTGTGTGGGGTTAAA 4860
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5001 GAAAAAGTAAAAAGATTTATCTGATGAAGAAAGAAACATTAGCTAAACTTGGTGTAAGT 5060
                     4621 GCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTTACA 4680
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Sequence 6 from patent US 5549897.
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1321 GGCAAGCTGATGATTACAGGCGATAAAGTCACATTAAAAACAGGTGCAGTTATCGACCTT 1380 1081 ATANTAAACCCAACCATTACTTACAGCATTGCCGCGCCTGAAAATGAAGCGGTCAATCTG 1140 1201 GGTAAACTTTCTGCTGATTCTGTAAGCAAAGATAAAAGCGGCAATATTGTTCTTTCCGCC 1260 1261 AAAGAGGGTGAAGCGGAAATTGGCGGTGTAATTTCCGCTCAAAATCAGCAAGCTAAAGGC 1320 1761 GGCAAGCTGATAAAGTCCGATAAAGTCACATTAAAAACAGGTGCAGTTATCGACCTT 1820 1401 ACTGTCGGTAAAGACGGCAGTGTAAATCTTATTGGTGGCAAAGTGAAAAACGAGGGTGTG 1460 1021 ATTAGCGTAAATGGTGGCAGCATTTCTTTACTCGCAGGCAAAAAATCACCATCAGCGAT 1080 981 CAATCTGTTTTAGCAAGCGGCAATTTAACATCGACCAAAATGAAATGGTGCAGTTTTTAC 1040 1020 781 GGACAAGTCTTTTTAATCAACCCAAATGGTATCACAATAGGTAAAGACGCAATTATTAAC 840 841 ACTAATGGCTTTACGGCTTCTACGCTAGACATTTCTAACGAAAACATCAAGGCGCGTAAT 900 541 CAATCTGTTTTAGCAAGCGGCTTACAAGGAATGGATGTAGTACACGGCACAGCCACTATG 600 741 GAACGCAAATGATAAAGTAATTTTAATTGTTCAACTAACCTTAGGAGAAATATGAACAAG 800 421 CGGGGTTGTGACCATTCCACAGAAAAGGCTTCCGCTATGTTACTATCTTTAGGTGTAAC 480 481 CACTTAGCGTTAAAGCCACTTTCCGCTATGTTACTATCTTTAGGTGTAACATCTATTCCA 540 961 ACTGTCGGTAAAGACGCCAGTGTAAATCTTATTGGTGGCAAAGTGAAAAACGAGGGTGTG

1500	56	1620	1680	1740	1800	1860	1920 2360	1980	2040	2100	2160	2220	2280	340	1400	460	520
ATTAGCAAGAAAACCTCTTTAGAAAAGGCTCAACCATCAATGTATCAGGC 	SGACGCGCTATTGTGTGGGGCGATATTGCGTTAATTGACGCCAATATT	AAGGTAGTGGTGATATCGGTAAAACCGGTGGTTTTGTGGAGACATCGGGGCAT 1 	CATTGACAGCAATGCAATTGTTAAAACAAAAGAGTGGTTGCTAGACCCTGAT :	CAATTGAAGCCGAAGACCCCTTCGCAATAATACCGGTATAAATGATGATTC 1 	CACCGGTGAAGCAAGCGACCCTAAAAAAATAGCGAACTCAAAACAACGCTA 	CAACTATTTCAAATTATCTGAAAACGCCTGGACAATGAATATAACGGCATCA 1 	TACCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATTCTCCAT 1 	CAGCGTGGCGGAGGGTTCAGATTGATGGAGATATTACTTCTAAAGGCGGG 	CATTTATICIGGCGGATGGCTTGATGTTCATAAAAATATTACGCTIGATCAG 2 	AAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 2	CAAATGCTAAAATTGTCGCCCAGGGCACTGTAACCATTACAGGAGAGGGAAA 2: 	GGTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 2 	AATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACA 2 	AACTACGAGAAAAGAACACCTCGTATTGGCAAACCAGCCATGATTCGCACTGG 2: 	GCTCTTAAPCTAGACACAGCGCAAATTTACCTTTATTAAATACATTTCA 2	CAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGC 24 	AAAA 2:
GGCATTCA           GCATTCA	AAAGAAAA          AAAGAAAA	AACGCTCA          AACGCTCA	TATTTATC          TATTTATC	GATGTAACA	CCAACAGG 	ACCAATACA              ACCAATACA	AGAAAACTI             AGAAAACTI	AGTAAAGGT 	AATTTAACÓ 	GGTTTTTTA 	GACGCGGCA 	GATTTCAGG	TCAGTGAAT.	ATTAACCAA 	AACGTCAGT	AGCAATAGC                AGCAATAGC	GTAAATGGC/           GTAAATGGC/
1441	1501	1561	1621	1681	1741	1801	1861	1921	1981	2041	2101	2161	2221	2281	2341	2401	2461 0
Qy Db	Oy Dp	Qy	Oy Dp	OY Db	Qy	Oy Dp	Oy Dp	Qy Dp	Oy Dp	Qy Db	Oy Dp	Qy Db	Qy Db	Qy	Qy Db	Qy Dp	Qy Dp

CCAAACGAGAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACA 2580 2700 3140 2760 2820 2880 2940 3000 3440 3060 3120 3560 3180 3620 3240 3680 3740 3360 3420 3601 AATGTTAAAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTG 3660 GTTCGCGGCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCA GAGTTAAAAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCCCAT AGCAGCAGCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCC AATTCAACCTACAACATATCCATTCTGGGGGGTAATGTCACCCTTGGTGGACAAAACTCA AATTTCAGCCTCAGACAGACGAAAGATGATTTTTATGACGGGTACGCAACGCAATGCCATC AATAACGCCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC GTTAATGGGAGTTTAAGTTTAACTGGCGAAAATGCAGATATTAAAGGCAATCTCACTATT TCAGAAAGGGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATCACGGCAATTTT ACCAATAATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTT ACCAATGATGGTGATTTAAACATTACCACTCACGCTAAACGCAACCAAAGAAGCATCATC TCAGATGCGACAAGTAATGCCAACCTAACTATTAAAACCAAAGAATTGAAATTGACAGAA GAAATCCAAATTGGCGGCAATATCTCGCAAAAAGAAGGCAACCTCACGATTTCTTCCGAT GACCTAAGTATTTCAGGTTTCAATAAAGCAGAGTTACAGCCAAAGATGGTAGAGATTTA ACTATTGGCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTTAAC 2961 2641 2701 3141 2761 3201 2821 3261 2881 3321 2941 3441 3381 3001 3501 3121 3181 3241 3681 3741 3061 3561 3621 3301 3361 3801 3421 3981 3481 3541 g ŏ g ŏ g pp qq ò Q ò g ò g δ q Ω ΩD ŏ δ ŏ q q ò ò g ò Pp ò g ò g QQ ò δy a ò

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                                                                                                         3901 GTTAGCGCGACTGGTGATTTAACCACTAAATCCGGCTCAAAAATTGAAGCGAAATCGGGT 3960
                                                                                                                                              3781 ACCGCGTCGGAAAAGGTTACCACCACCAGCAGCTCGACCATTAACGCAACAAATGGCAAA 3840
                                                                                      3721 ATTACTGCAAAAAATGTAGAAGTAAACAAAGATATTACTTGTCTCAAAACAAAATATC 3780
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                                                                                                                                                                                                                                         High molecular weight surface proteins of non-typeable haemophilus Patent: US 5603938-A 6 18-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           741 GAACGCAAATGATAAATTTAATTGTTCAACTAACCTTAGGAGAAATATGAACAAG 800
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            5121 ACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTAAT 5180
                                                                                                                                                                                                                                                                                                       97.6%; Score 4820.2; DB 6; Length 9323; 98.5%; Pred. No. 0;
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0; Mismatches 73; Indels
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1. .9323
                                                                                                                                                                                                                                                                            /organism="unknown"
1829 c 1832 a
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Barenkamp, S.J.
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                                                                                                               4921 AACAGGTTATTATTATG 4937
                                                                                                                        5361 AACAGGTTATTATTATG 5377
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Matches 4864; Conservative
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2001 AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGAGACACATCGGGGCT 2060 1561 AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGGAGACATCGGGGCAT 1620 1621 TATTTATCCATTGACAGCAATGCAATTGTTAAAACAAAAGAGTGGTTGCTAGACCCTGAT 1680 1681 GATGTAACAATTGAAGGCGGAAGACCCCCTTCGCAATAATACGGGTATAAATGATGAATTC 1740 1741 CCAACAGGCACCGGTGAAGCAAGCGACCCTAAAAAAATAGGGAAGTCAAAACAACGCTA 1800 1801 ACCAATACAACTATTTCAAATTATCTGAAAACGCCTGGACAATGAATATAACGGCATCA 1860 1861 AGAAAACTTACCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATTCTCCAT 1920 1921 AGTAAAGGTCAGCGTGGGGGGGGTTCAGATTGATGBAGATATTACTTCTAAAGGCGGA 1980 1981 AATTTAACCATTTATTGTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG 2040 2421 AATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATGAG 2480 1481 GGTTTTTAAATATACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCC 2540 2041 GETTITITAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 2100 2101 GACGCGGCAAATGCTAAAATTGTCGCCCAGGGCACTGTAACCATTACAGGAGAGAAAA 2160 2601 GATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAACGTCTGAATATCATTTCA 2660 2161 GATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 2220 2221 TCAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTAACATATGTGGGAATATAACA 2280 2661 TCAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTHIIIIIIIIIIIIIIIIIIIIIII 2281 ATTAACCAAACTACGAGAAAGAACACCTGGTATTGGCAAACCAGCCATGATTCGCACTGG 2340 2721 ATTAACCAAACTACGAGAAAGAACACCTCGTATTGGCAAACCAGCCATGATTGGCAACCAGCATGGTTGGCAACTGG 2780 2341 AACGTCAGTGCTGTTAATCTAGAGAGAGGCGCAAATTTTACGTTTATTAAATACATTTCA 2400 2781 AAGGTCAGTGCTCTTAATCTAGAGACAGGCGCAAATTTTACCTTTATAATAATACATTGA 2840 2901 GTANATGGCAACATGTCATTCAATGTCAAGAAGAGGGGGAAAGTTTCAATTTCAATTTAAA 2960 2461 GTAAATGGCAACATGTCATTCAATCTCAAAGAAGGAGGGAAAGTTAATTTCAAATTAAAA 2520 2521 CCAAACGAGAACATGAACACAAGCAAACTTTACCAATTCGGTTTTTAGCGAATATCACA 2580 2401 AGCAATAGCAAAGGCTTAACAACACAGTATAGAAGCTGTGAGGGGTGAATTTTAACGGC Op ŏ ò DP ö Db αq ò õ q ŏ g ò q qq δ ò qq ò q qq ò g ò Db à QQ à Op

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. X 6	761 AATTTCAGO	CAGACAGAGGAAAGATGATTTTTATGACGGGTACGCACGC
3 2 6	821 AATTCAACCTP	CAACATATCCATTC
3 6	2881 AGCAGCAGCAT 1	TACGGGTACGGGTACGGGGGGGGGGGGGGGGGGGGGGGG
3 6	2941 AATAACGCCC	4 - 4
o y	3001 GTTAATGGGA	FTTAAGTTTAAC
a à	3061 TCAGAAAGC	CACTITITAAAGGAAAGACTAGAGATACO CACTITITAAAGGAAAGACTAGAGATACO
oy Oy	3121 ACCAATAAT	GCACTGCCGAAATTAATATAACACAAGGA GCACTGCCGAAATTAATATAACACAAGGA
ag A	3561 ACCAATAAT 3181 ACCAATGAT	GCALISCOSSANIA GTGATTTAAACATTACCACCACGCTAAACGCAP GTGATTTAAAACATTACCACTCACGCTAAACGCAP
g ko	3241 GGCGGAGAT 	ATCAACAAAAAGGAAGCTTAAA
o o	3301 GAAA1	rggcggaatatcgcaaaaagaaggcaacc
d ç	3741 GAAATCCA 3361 AAAATTAA	TOCCOSCENTIAL OF COATCAAAAGGGTATTGATGGA CACCAAACAGATAACAATCAAAAAGGGTATTGATGGA 
og og	3421 TCAGATGC	AAGTAATGCCAACTAATAAAACCAAAG AAGTAATGCCAACTAATAAAACCAAAG ACTAAATAAACTAAAC
වූ ද	3481 GACCTAAG	ACENTIALICOGRADO ATTICAGGITTCAATAAGGAGAGAGATACAGCCAAAG
ă ă î	3541 ACTATIGG	AACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTTAAC 3 AACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTTAAC 4 AACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTTAAC 4
5 6	3601 AATGTT	FCAAAATCTCTGCTGACGGTCACAATG
ā õi	AAAAC!	AGCAATGGCGGACGTGAAAGCAATAGCGAC
Δ C	CATC	TAGCAGCAATGGCGGACGTGAAAGCAATAGCGACAACAAAAAAGTAACOGTTTTTAAAAAATGTAAAAAGTAAATATC 378
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4801 GTAGATTTCATCCTGCAATGAQTCATTTTATTTTCGTATTATTTACTGTGTGGGTTAAA 4860 4741 GGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACAAG 4800 4621 GCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTACA 4680 4681 ACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTAAT 4740 4501 AARTATGCGGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCCTT 4560 4561 GAAAAAGTAAAAGATTTATCTGATGAAGAAAGAGAAACATTAGCTAAACTTGGTGTAAGT 4620 4441 AATAICATITCGAAAGAIGGIAGAAACACIGIGCGCIIAAGAGGCAAGGAAAITGAGGIG 4500 4381 ACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGTTA 4440 4321 GATGCATCAGGTGATAGTACAGAAGTGAATGCAGTCAACGCAAGCGGCTCTGGTAGTGTG 4380 4261 GATATTAAAGCAACCAGCGGCACCTTGGTTATTAACGCAAAAGATGCTAAAGCTAAATGGT 4320 4141 ATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAAGC 4200 4201 ATTAAIGCTGCTAAIGTGACAJTAAATACTACAGGCACCTTAACCACCGTGGCAGGCTCG 4260 4080 4140 3961 GAGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGGTA 4020 3901 GTTAGCGCGACTGGTGATTTAACCACTAAATCCGGCTCAAAAATTGAAGCGAAATCGGGT 3960 3841 GCAAGTAFTACAACCAAAACAGGTGATATCAGCGGTACGATFTCCGGTAACACGGTAAGT 3900 4021 AATGITACGGCAAACGCTGGCGATTTAACAGTTGGGAATGGCGCAGAAATTAATGCGACA 4081 GAAGGAGCTGCAACCTTAACCGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCTAGC οý qq δý δλ qq δý Dp qq δλ g δy q δλ q Dp οy g δ ΩQ ò δy QΥ g g òγ g δ Dp δý qq

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                                                                                                                                                                                            High molrcular weight surface protein of non-typeable haemophils Patent: JP 2001503602-A 4 21-MAR-2001; SENTLOUIS UNIV, WASHINGTON UNIV
4861 GITCAGTACGGGGTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTTT 4920
                         61 CACCTTTTTGCAGTCTATATGCAAATATTTTAAAAAATAGTATAAATCGGCCATATAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AATGGTATAATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTTCAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97.6%; Score 4817; DB 6; Length 9323;
98.5%; Pred. No. 0;
Live 0; Mismatches 75; Indels 0;
                                                                                                                                                                                                                    Haemophils
JP 2001503602-A/4
21-MAR-2001
01-APR-1997 JP 1997535346
01-APR-1996 US 08/617697
STEPHEN J BARENKAMP
CO7H21/02,CO7H21/04,C12P21/06,A61K39/102
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1828 c 1833 g 2528 t

    9323
    organism="unidentified"

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/organism='Haemophils'.
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                                                 4921 AACAGGTTATTATTATG 4937
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Barenkamp, S.J.
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BD010358
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                                                                          481 CACTTAGCGTTAAAGCCACTTTCCGCTATGTTACTATCTTTAGGTGTAACATGTATTCCA 540
                                                                                      541 CAATCTGTTTTAGCAAGCGGCTTACAAGGAATGGATGTAGTACACGGCACAGCCACTATG 600
                                                                                                                                                             601 CAAGTAGATGGTAATAAAACCATTATCCGCAACAGTGTTGACGCTATCATTAATTGGAAA 660
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Db 186 Qy 150 Db 194 Qy 156 Qy 165	Db 206 Qy 168 Db 211 Qy 17 Db 21	22 18 25 19 20 20 20 20 20 20 20 20 20 20 20 20 20	00 2 00 2 00 00 00 00 00 00 00 00 00 00	60 60 60 60 60 60 60 60 60 60 60 60 60 6

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64 64 64 64 64 64 64	oy oy oy	D Cy			

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HIU08876 9221 bp DNA linear BCT 05-AUG-1994 Raemophilus influenzae 12 adhesin (hmw.lA) gene and putative accessory processing proteins (hmw.lB) and (hmw.lC) genes, complete cds.
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Submitted (14-APR-1994) Stephen J. Barenkamp, Department of
Pediatrics, St. Louis University School of Medicine, Cardinal
Glennon Children's Hospital, 1465 South Grand Boulevard, St. Louis,
MO 63104-1095, USA
On Apr 29, 1994 this sequence version replaced gi:148902.
4801 GTAGATTTCATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTACTGTGTGGGTTAAA 4860
                                                                                                                       5241 GTAGATTTCATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTACTGTGTGGGGTTAAA 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barenkamp, 3.7 and Leininger, E. Cloning, expression, and DNA sequence analysis of genes encoding nontypeable Haemophilus influenzae high-molecular-weight surface-exposed proteins related to filamentous hemagglutinin of Infect. Immun. 60 (4), 1302-1313 (1992)
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Haemophilus influenzae
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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Barenkamp, S.J. and St Geme, J.W. III.
Genes encoding high-molecular-weight adhesion proteins of
nontypeable Haemophilus influenzae are part of gene clusters
Infect. Immun. 62 (8), 3320-3328 (1994)
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                                                             41 ATGACAAACAACAATTACAACACCTTTTTTGCAGTCTATATGCAAATATTTAAAAAAT 100
                                              Ouery Match 54.5%; Score 2689.8; DB 1; Length 9221;
Best Local Similarity 73.6%; Pred. No. 0;
Matches 3767; Conservative 0; Mismatches 1087; Indels 265; Gaps
                                                                                                                                                                                                                                            581 TACACGGCACACCACTATGCAAGTAGATGGTAATAAAACCATTATCCGCAACAGTGTTG
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1	qq	35
J	δ,	357 ATCTAGAGACAGGCGCAAATTTTACCTTTATTAAATACATTTCAAGCAAAGAAAA
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δλ	7	708 GCGAIGACGCITITAAAAICAACAAAGACITAACCAIAAAIGCAACCAAATTTAAATTAAA
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<u>&gt;</u>	3068	GCGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATTACCCCAAATTACCCAAAATAAAATAAT
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O.Y	3188	atgetgatttaaacattaccactcacgtaaacgcaacaaaaaaagcafcafcggggg 324/ 	
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1 (bases 1 to 5116)
Barenkamp,S.J. and St. Geme,J.William. III.
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High molecular weight surface proteins of non-typeable haemophilus Patent: US 5869065-A 1 09-FEB-1999;
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	δλ	2069 T	GAAGGTGGAAATAACAAAGCACGCGACGCGAAATGCTAAAATTGTCGCCC 212
	qq	2074 A	AGATATCGCCTTTGAGAAAGGAAGCAACCAAGTCATTACAGGTC 2118
	Qy.	σ (	AGGCCACTGTAACAGTACAGGAGAGGGAAAAGATTTCAGGGCTAACAACGTATCTTAA 2188
	g	2119 A	177
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	ογ	0	CAATCTTAGTGGCACAATTAACATATCTGGGAATATAACAATTAACCAAACTACGA 2296
	qq	2236 A	ATAAATTTGAAGGGACTTTAAATATTTCAGGGAAAGTGAACATCTCAATGGTTTTACTA 2295
	δλ	2297 G	10
	οp	2296 A	235
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	οy	2414	47
	qq	2416	247
	οy	2474	53
	qq	2473	ITAATGTTGAACGAAATGCAAGAGTCAACTTTGACATCAAGGCACCAATAGGGATAAATA 2532
	δλ	2534	TGACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACAGCCACTGGTGGGG 2593
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	δγ	2594 (	GCTCTGTTTTTTTGATATATATGCCAACCATTCTGGCAGAGGGCTGAGTTAA 2647
	qq	2593 (	STGTTGATTTCACACTTCTCGCCTCATCCTCTAACGTCCAAACCCCCGGTGTAGTTATAA 2652
	δ	2648	AAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCCCATGTTCGCG 2707
	QΩ	2653	ATTCTAAATACTTTAATGTTTCAACAGGGTCAAGTTTAAGATTTAAAACTTCAGGCTCAA 2712
•	. Оу	2708	GCGATGACGCTTTTAAAATCAAAGACTTAACCATAAATGCAACGAATTCAAATTTCA 2767
	QQ	2713	CAAAAACTGGCTTCTCAATAGAGAATTTAACTTTAAATGCCACCGGAGGCA 2766
	Qy	2768	GCCTCAGACAGACGAAAGATGATTTTTATGACGGGTACGCACGC
	QQ	2767	acataacacttttgcaagttgaaggcaccgatggaatgattggtaaggcattagcca 2826
	οy	2828	CCTACAACATATCCATTCTGGGGGGTAATGTCACCTTGGTGGACAAAACTCAAGCAGCA 2887
	qq	2827	28
	δ	2888	GCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCCAATAACG 2947
	QQ	2887	AAATCGAAGGCAATGTTACTATCAATAACAACGCTAACGTCACTCTTATCGGTTCGGATT 2946
	Οy	2948	CCCCTAATCAGCAAAACATAAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTCGTTAATG 3007
	qq	2947	
	Qy	3008	GGAGTITAAGTITAACTGGGGAAAATGCAGATATTAAAGGCAATCTCACTATTTCAGAAA 3067
	qq	3001	æ
	οy	3068	GCGCCACTITIAAAGGAAAGACIAGAGAIACCCTAAAIAICACCGGCAATITIACCAAIA 312;
	qa	3061	

4197	GCGGGCCTAACGTAACAAGTGCAACAGGTACAATTGGTGGTACGATTTCCGGTAATACGG	4138	Dp
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3839	CGGAAAAGGTTACCACCACACCACGACCATTAACGCAACAAATGGCAA	3788	δy
3777	CAAAAAATGTAACAGTAAACAACAACAATTACTTCTCACAAAGCAGTGAGCATCTCTGGA	3718	qq
3787	CAAAAAATGTAGAAGTAAACAAAGATATTACTTCTCTCAAAACAGTAAATATCACCGCGT	3728	δλ
3717		3658	Db
3727	CTAGCAGCAATGGCGGACGTGAAAGCAATAGCGAAACGATACCGGCTTAACTATTACTG	3668	λ
65	ARGATTCAAAATCTCTGCTGACGGTCAAATGTGAAALTAAATAAAAATAAAAAAAAAA	3608	λ 2
	GTAACACCAATAGTGCTGATGGTACTAATGCCAAAAAAGTAACCTTTAACCAGGTTA	3541	g
9	GCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTTAACAATGTTA	3548	λλ
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3547	GTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTAACTATTG	3488	χχ
3480	CGACAGTAATGCCAACCTAACTATTAAAACCAAAGATTGAAATTGAAATTGAAAAANAACLAA 	3428	ž ą
42	ATAITACCAAACAGATAACAATCAAGGCAGGTGTTGATGGGGAGAATTCCGATTCAGACG	3361	ą
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                                                  GCATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAA 4198
                                                                                           GCATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGCT 4258
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Search completed: March 22, 2003, 00:41:58 Job time : 12519 secs

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(without alignments)
12231.150 Million cell updates/sec
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                                                                                                                                                                                                                                                                                      March 21, 2003, 15:43:31; Search time 909 Seconds
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Non-typeable Haemo	Sequence encoding	Haemophilus influe	Haemophilus high m	Gene cluster for h	Non-typeable Haemo	DNA encoding Haemo	Sequence encoding	Haemophilus high m
	a	AAT90995	AAQ49507	AAA52197	AAQ72294	AAQ49509	AAT90997	AAA52198	AAQ49506	AA072293
		18	14	21	15	14	18	21	14	ŗ
	Length	4937	4937	4940	4937	9323	9323	3263	5116	5116
æ	Query Match	100.0					97.6	66.1	54.3	7
	Score	4937	4935.4	4924	4913	4828.2	4820.2	3263	2680.2	2600 2
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	જ	% Query Score Match Length DB ID	Score Match Length DB ID DATE	Score Match Length DB ID 4937 100.0 4937 18 AAT90995 4935 4 100.0 4937 14 AAQ49507	Score Match Length DB ID 4937 100.0 4937 18 AAP90995 4935.4 100.0 4937 14 AAQ49507 4936.9 99.7 4940 21 AAA52197	Score Match Length DB ID 4937 100.0 4937 18 AAP90995 4935.4 100.0 4937 14 AAQ49507 4943 99.7 4940 21 AAAAS197 4913 99.5 4937 15 AAO72294	Score Match Length DB ID  4937 100.0 4937 18 AAT90995 4935.4 100.0 4937 14 AAQ49507 4924 99.7 4940 21 AAA52197 4913 99.5 4937 15 AAA07294 4878.2 97.8 9323 14 AAQ49509	Score Match Length DB ID  4937 100.0 4937 18 AAT90995  4935.4 100.0 4937 14 AAA049507  4914 99.7 4937 15 AAA02197  4918 99.5 4937 15 AAA02294  4828.2 97.8 9323 18 AAA049997	Score Query DB ID D D D D D D D D D D D D D D D D D	Score Match Length DB ID  4937 100.0 4937 18 AAT90995 4935.4 100.0 4937 18 AAT90995 4913 99.7 4940 21 AAA52197 4913 99.5 4937 15 AAA52197 4820.2 97.6 9323 14 AAQ49509 4820.2 97.6 9323 18 AAT90997 2580.2 54.3 5116 14 AAQ49506

Non-typeable Haemo	philus i	Gene cluster for h		Non-typeable Haemo	Partial sequence e		a		-н -		-	DNA encoding H. 1n	DNA encoding Haemo	Haemophilus nign m	Partial sequence e	Haemophilus influe	encoding H.	DNA encoding H. In	Haemophilus infine	Haemophilus influe	encoding	DNA encoding Haemo	-	encoding	DNA encoding Haemo	н.	DNA encoding B. In	Haemophilas Intia	Haemophilus iniue	DNA encoaing H. III	Presilita DS-1200 5	Drosophita meranog	Haemophitus intide	Prasmin Contractor	
AAT90994	AAA52195	AA049508	AAT90996			AA07229			-					AAQ72295							AAA52190			-	AAA52194	AAA5219	AAA5218	AAA5217	AAA5217	AAA5217	AAA5216	ABL18982	AAT420	AAA521	AAH44801
8	7	4	8	18	14	15	18	21	21	21	21	21	21	15	14	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	23	٦.	21	22
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5.4.3	. 45	. 42	22.0	4.5	44.6	44.6	0.0	30.0	35.5	30.4	30.3	30.1	30.0	29.8	29.8						23.7					15.3									
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## LIGNMENT

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Non-typeable Haemophilus high mol.wt. surface protein hmw2 gene.
                                                                                                                Non-typeable Haemophilus; high molecular weight surface protein; HMW2; hmw2 gene; immunogen; vaccine; otitis media; ss.
                                                                                                                                                                                                   Location/Qualifiers
341..345
                                                                                                                                                                                                                                      /*tag= a
129..135
/*tag= b
/rpt_type= TANDEM
136..142
                                                                                                                                                                                                                                                                                                                                                                                /rpt_type= TANDEM
150..156
                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= e
/rpt_type= TANDEM
157..163
                                                                                                                                                                                                                                                                                                                     /*tag= c
/rpt_type= TANDEM
143..149
                                                                                                                                                                     Haemophilus influenzae strain 12.
AAT90995 standard; DNA; 4937 BP
                                                            14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
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                                 AAT90995;
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cept (pos 465, 485), aa Sk

cept (pos 467, 462, aa Lys

cept (pos 460, 462, aa Pro)

cept (pos 466, 468, aa Ala)

ppt (pos 466, 468, aa Ala)

ppt (pos 472, 471, aa Bet)

pt (pos 472, 474, aa Lys)

cept (pos 478, 480, aa Lys)

cept (pos 172, 147, aa Val)

cept (pos 1621, 162)
                                                                                                       /rpt_type- TANDEM
171..177
          /rpt_type= TANDEM
164..170
                                                                                                                                                                                                              'rpt_type= TANDEM
.78..184
                                                                                                                                                                                                                                                                                                                  /rpt_type= TANDEM
185..191
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92..198
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199..205
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206..212
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227..233
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220..226
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234..240
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352..4785
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pos:1636..1638, aa:Asp)
pos:1651..1653, aa:Asp)
pos:1654..1656, aa:Ala)
pos:1675..1677, aa:Phe)
                                                                                                                                                 /transl_except= (pos:1693..1695, /transl_except= (pos:1711..1713,
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[pos:1681..1683, aa.Asn]
[pos:1687..1689, aa.Ser]
[pos:1693..1695, aa.Asn]
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aa: Lys)

Barenkamp SJ;

WPI; 1997-503038/46. P-PSDB; AAW30294.

```
This nucleic acid comprises the hmw2 gene of non-typeable
Haemophlus influenzae strain 12 that encodes high molecular
Weight surface protein 18M2 (see AAW30294). A phage genomic
library of strain 12 was screened for clones expressing high
Strongly reactive clones were subcloned into T7 expression
Strongly reactive clones were subcloned into T7 expression
blasmid; all expressed either 120 kba HMW2 or 125 kba HMW1 (see
AAW30293). The expressed proteins are truncated, starting at
residue 442 of both full-length HMW1 and HMW2 gene products.
Correct processing requires the products of additional
correct processing requires and peptides can be used in
correct process or ne used as to prepare recombinant proteins and as
correct processing requires for prepare recombinant proteins and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CACCTTTTTGCAGTCTATATGCAAATATTTTAAAAAATAGTATAAATCCGCCATATAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGTAGATGGTAATAAAACCATTATCCGCAACAGTGTTGACGCTATCATTAATTGGAAA 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 ATATATCGTCTCAAATTCAGCAAACGCCTGAATGCTTTGGTTGCTGTGTGTAATTGGCA
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High molecular weight proteins of non-typeable Haemophilus influenzae - useful for vaccine production
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4937 BP; 1729 A; 948 C; 1009 G; 1251 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Prec. ...
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                                                Claim 7; Page 71-73; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 4937; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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ACAACG	ACGGCA IIIII	ATTCTC 	AAAGGC 	CTTGA1	AAAGC	AGAGGG	FATCAT	SAATAT            SAATAT	TTCGCA          TTCGCA	ATACAT            ATACAT	TTTTA	CAAAT	CAATA	SCAGAG              CAGAG	raaati 11111 raaati	CAACCA	GCAATG	GACAA
TCAAA! TCAAA!	ATATA         ATATA	ACTTA 	ACTTCT               ACTTCT	ATTACG 	AATAAC 	ACAGGA               ACAGGA	CTGAA? 	TCTGG          TCTGG	CATGA	FATTAA               FATTAA	SGTGAA          SGTGAA	TAATT        TAATT	TTTAGG	TTCTG	TACCT	AAATG	ACGCAC	TGGTG
CGAAC 	AATGA	ACTCCC	ATATI          ATATI	AAAAT	GTGGA         GTGGA	CCATT	AAAGGT 	AACATA	ACCAGO ACCAGO	ACCTT	GCAGG           GCAGG	AAAGT	CGGTT	AACCA 11111 AACCA	FAATT 	AACCAT HIIIII AACCAT	CGGGT1	CACCC
AAATAG 	CTGGAC	AAGCA          AAGCA	TGGAG 	TCATA	TTGAAG         TGAAG	CTGTAP	CGGGT4 11111 CGGGT4	CAATT	GGCAA 11111 GGCAA	ATTTT 	AGCTCT         GCTCT	SGAGCG 11111 SGAGCG	CCAAT	FATGCC IIIII TATGCC	96CGC	GACTT	TATGA	AATGT
AAAAA 	AACGC	ATCGG 	SATTGA         SATTGA	rGATG1         rGATG1	AGCTT1	GGGCAC        GGGCAC	CGGAA         CGGAA	TGGCA TGGCA	GTATT	SCGCAA 11111 SCGCAA	ATAGAP ATAGAP	AAGAAC               AAGAAC	CTTTAC         CTTTAC	ATATA 	CTAAC	ACAAA ACAAA	SATTTI	3GCGG1
ACCCT 1111 ACCCT	TGAAA	ATCAAC ATCAAC	GTTCAC GTTCAC	TGGGT       TGGGT	TCCGT	GCCCA	TTAAA 	CTTAG	CACCTC	GACAGO GACAGO	ACAGT ACAGT	TCTCA	CAAAC	TTTTG	ATATCI 	AAATCA          AAATCA	AAGATC	TTCTG
CAAGCG	ATTATC         ATTATC	GCTCA	GAGGC	GCGGA 11111 GCGGA	SCCGCT	ATTGTC	STATC1            GTATC1	CACAA?	AAGAA(        AAGAA	CTAGA	ACAAC	ATTCAA 	CACAAG	rgrrri        rgrrri	AATTAJ 	TTTTA 	GACGA	GACGA
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ACCGG 	ACTAT	raccgi IIIIII raccgi	rcagco rcagco	CATTY CATTY	AAATA'        AAATA'	AAATG	GGCTA	TAATT	AAACTA	STGCTC	GCAAA(        GCAAA(	GCAAC              GCAAC	AGAAC 	GTGGG	AAAATG	SGCGAT 11111 SGCGAT	AGCCTC	AGCCTC
ACAGGC IIIII	AATACA AATACA	AAACT	AAAGG         AAAGG	TTAAC	TTTTT:	090090	rrrcaG	AGTGA/ 	TAACC	CGTCA	CAATA	AAATG	AAACG	CCACTO	AGTTAA          AGTTAA	TTCGC(	ATTTC	ATTTC
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3901 GTTACCGCCACTGGTGATTTAACCACTAAATCCGGCTCAAAATTGAAGCGAAATCGGGT 3960 3961 GAGGCTAATGTAACAAGTGCAACAGTACAATTGGCGGTACAATTTCCGGTAATACGGTA 4020 4021 aatettacgecaaacgetggegatttaacagttgggaatggegeagaaattaafgegaca 4080 4081 GAAGGAGCTGCAACCTTAACCGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCTAGC 4140 4201 ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGTTG 4260 4261 GATATTAAAGCAACCAGGGCACCTTGGTTATTAACGCAAAAGATGCTAAGCTAAATGGT 4320 4381 ACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGTTA 4440 4441 AATATCATTTCGAAAGATGGTAGAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGGTG 4500 4501 AAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCCTT 4560 4561 GAAAAAGTAAAAGATTTATCTGATGAAGAAAGAGAAACATTAGCTAAACTTGGTGTAAGT 4620 4621 GCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTTACA 4680 4681 ACCAGACCGTCAAGTCAAGTGATATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTAAT 4740 GGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACAAG 4800 4801 GTAGATTTCATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTACTGTGTGGGTTAAA 4860 4861 GTTCAGTACGGGCTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTT 4920 4861 GTTCAGTACGGGCTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTTT 4920 4141 ATCACTICAACTAAGGGICAGGIAGACCICITGGCICAGAAIGGIAGCAICGCAGGAAGC 4321 GATGCATCAGCTGATAGTACAGAAGTGAATGCAGTCAACGCAAGCGGCTCTGGTAGTGTG 4921 AACAGGTTATTATTG 4937 4921 AACAGGTTATTATG 4937 ò q δ 셤 δ QQ ò q qq à ŏ g δλ qq ò qq QQ ò ò qq ò g QΩ ò g ó ò q ò a ò qq δ

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HMW; high molecular weight protein; virus; vaccine; influenza; epitope; immunity; haemophilus influenzae; Ss.
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/transl_except= AAA encodes Aspartic acid.
misc_difference 1654..1656
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/rransl_except= TCC encodes Phenylalanine.
misc_difference 1633..1635
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/transl.except= AGC encodes Aspartic acid
/fransl.except= AGC encodes Aspartic acid
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                                                                                                                                                                                                                                                             /*tag= c
/transl_except= CGC encodes Glutamic acid.
misc_difference 457...459
                                                                                                                                                                                        /product High molecular weight protein 2.misc_difference 451..453
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//ransl.except= GAT encodes Asparagine.
misc_difference 1687..1689
/*tag= t
                                                                        Sequence encoding high molecular weight protein 2 (HMW2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_except= TTT encodes Methionine misc_difference 472..474
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/transl_except= AAC encodes Argenine.
misc_difference 1621..1623
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/transl_except= ATC encodes Argenine.
misc_difference 469..471
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/transl_except= ACA encodes Alanine.
misc_difference 1675..1677
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/transl_except= GTT encodes Proline.
463..465
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/transl_except= GAC encodes Lysine.
misc_difference 1636..1638
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/transl_except= TAT encodes Lysine.
misc_difference 460..462
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misc_difference 478..480
                                                                                                                                                                                                                                 /trainsl_except= TTC encodes Serine.
misc_difference 454..456
                                                                                                                                                                    Location/Qualifiers
AAQ49507 standard; DNA; 4937 BP
                                                     26-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                             Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                   misc_difference 463
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                              AAQ49507
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361 ATATATCGTCTCAAATTCAGCAAACGCCTGAATGCTTTGGTTGCTGTGTCTGAATTGGCA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GAACGCAAATGATAAATTTAATTGTTCAACTTAAGGAGAAAATATGAACAAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The isolation and purification of the high molecular weight protein enables the identification of the major protective epitopes of the protein by conventional epitope mapping. These epitopes can then be synthesised using standard techniques and incorporated into fully synthetic or recombinant vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 4935.4; DB 14; Length 4937; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 1; Indels 0; Gamatches 4936; Conservative 0; Mismatches 1; Indels 0; Gamatches 10; Gamatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4937 BP; 1729 A; 947 C; 1010 G; 1251 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High molecular weight surface proteins - of non-typeable haemophilus which exhibit immunogenic properties
/transl_except= ACA encodes Serine.
misc_difference 1693..1695
/transl_except= GAA encodes Asparagine.
misc_difference 3913..3915
                                                                                                                                                               /transl_except= GGT encodes Valine
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P-PSDB; AAR41724.
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8	541 CAATCTGTTTTAGCAAGCGGCTTACAAGGAATGGATGTAGTAC	TACACGCACAGCCACTATG 60
ă ô	AATCTGTTTTAGCAAGGGTTACAAGGAATGGATGTAGTAC AACTAACAACAACGAATGGATGTAGTAC	STACACGG
7 20	601 CAAGTAGATAAAAACCATTATCCGCAACAGTGTTGACG	CGCTATCATTAATTGGAAA 6
ογ	661 CAATTTACATCGACCAAAATGAAATGGTGCAGTTTTTACAA	AAAACAACAACTCCGCC 720
පි	661 CAATTAACATCGACCAAAATGAAATGGAGTGCAGTTTTACAA	
o d	721 GTATTCAACCGTGTTACATCTAACCAATCTCCCAATTAAAAGG 721 [11] [11] [11] [11] [11] [11] [11] [1	ATTTTAGATTCTAAC 78
ò	781 GGACAACMCMMMM1317011011010101010101010101010101010101	ATTITAGATICIAAC 78
7 dd	781 GGACAAGTCTTTTTAATCAACCCAAATGGTATCACAATAC 781 GGACAAGTCTTTTTAATCAACCCAAATGGTATCAAGAATAC	STAAAGACGCAATTATTAAC 8
δ	841 ACTAAIGGCTTTACGCCTTCTACGCTAGACATTTCTAACG	AAGGCGCGTAAT 90
QQ	841 ACTAATGGCTTTACGGCTTCTACGCTAGACATTTCTAAC	GAAAACATCAAGGCGCGTAAT 900
oy B	901 TTCACCTTCGAGCAAACCAAAGATAAAGCGCTCGCTGAAATT 	TTGTGAATCACGGTTTAATT 960
ò	961 ACMCMOCOMANA AND CONTRACT AND GEORGE CONTRACTOR	rgrgaarcacggrrraarr 96
3 8	901 M.TGLUGGTAAAGAGGGAAGTGTAAATCTTATTGGTGGAAAG: 	AAAAACGAGGGTGTG 102
δy	1021 ATTAGGGTAAATGGTGGCAGCATTTCTTTACTCGCAGGGCAAAA	ATCACCATCAGCGA?
q	1021 ATTAGCGTAAATGGTGGCAGCATTTCTTTACTCGAGGG	ō
οy	1081 ATAATAAACCCAACCATTACTTACAGCATTGCCGCGCC	AATCTG 114
QQ	1081 ATAATAAACCCAACCATTACTTACAGCATTGCCGCGCC	
٥y	1141 GGGGATATTTTGCCAAAGGCGGTAACATTAATGTCCG	AACCAA 120
QQ	1141 GGCGATATTTTGCCAAAGGCGGTAACATAATGTCCGTGCTGC	CACTATTCGAAACCAA 120
oy Op	1201 GGTAAACTTTCTGCTGATTCTGTAAGCAAAGATAAAAGGGGCAAN	ATTGTTCTTTCCGCC 126
οy	1261 AAAGAGGTGAAGCGGAAATTGGCGGTGTAAATTTCC	TITCGGC 126
QQ	1261 AAAGAGGTGAAGCGGAAATTGGCGGTGTAATTTCC	
δy	1321 GGCAAGCTGATGATTACAGGCGATAAAGTCACATTAA	TCGACCTT 138
Q .	1321 GGCAAGCTGATGATTACAGGCGATAAAGTCACATAAAAACACGT	STGCAGTTATCGACCTT 138
g g	1381 TCAGGTAAAGAAGGGGAQAAAACTTACCTTGGCGGTGACGAGGGC 	CGCGCCAAGCTAAAAC 144
ò	1441 GGCATTCAATTAGCAAAAAAAAAAAAAAAAAAAAAAAAA	CGGCGAAGGTAAAAAC 144
g 20	1441 GGCATTCAATAGCACAAAACCICTTAGAAAAGGCTCAAC	AACCATCAATGTATCAGGC 1500 
ΟŸ	1501 AAAGAAAAAGGGGACGCGCTATTGTGTGTGGGGCGATATTGC	ATTGACGCAATATT 156
g ,	1501 AAAGAAAAGGCGGACGCGCTATTGTGTGTGTGTGTGTGTG	56
ð ø	1561 AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGG	GTGGAGACATCGGGGCAT 1620

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TTTACCT  TATAAATG  TATAAATG  TATAAATG  TATACGCAC  TATACGCAC	AAA AAA IIII AAA IIAA	FAATTTCACCGGC 		GACAAGTAATGCCAACCTAATTAAAACCAAAGAATTGAAATT [	STGACP STGACP SACAAC SACAAC TCTCTC
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GAGTGAATTTGACGCTTTTTGACGCTTTTTTGACGCTTTTTTTT	CATTACGGGGAATATTACTA1	TTT TTT TTT GCC GCC	GATATAATCAACAAAAA	CCAAGTAATGCC CAAGTAATGCC TTTCAGGTTTC TTIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	"AAGATTCAAAATCTC"
AGTTAAAAA) TTCGCGGCG/ TTCGCGGCG/ TTCGCGCGCG/ ATTTCAGCCC ATTTCAGCC/ ATTCAGCC/ ATTCAACCT/ ATTCAACCT/	AGCAGCATTP	TCAGAAAGGGCCACT                  TCAGAAAGGGCCACT ACCAATAATGGCACT	GGCGGAGATATAA                             GGCGGAGATATAA   GAAATCCAAATTC                                   GAAATTAATACT   AAAATTAATATCA	TCAGATGCGACA 	TTA LII CAT CAT CAT CTG
2641 G 2701 G 2701 G 2761 A 2761 A 2761 A 2821 A	2881 A 2881 A 2941 A 2941 B 3001 G	3061 7 3061 7 3121 <i>i</i> 3121 <i>i</i> 3181 <i>i</i>	3241 3241 3301 3361 3361	3421 3421 3481 3481 3541	3601 3601 3661 3661 3721
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GGGTCGGAAAGGTTACCACCACAGCAG 	AAGTATTACAACCAAAACAGGTGATATCAGGGGTAC 	AGCGCGACTGGTGATTTAACCACTAAATCCGGC 	GCTAATGTAACAAGTGCAACAGGTACAATTGGC 	ACGGCAAACGCTGGCGATTTAACAGTTGG 	AAGGAGCTGCAACCTTAACCGCAACAGGGAATACCTTGA 	CACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATG 	TPATGCTGCTAATGTGACATTAAATACTACAGGCACCT 	TATTAAAGCAACCAGGGGACCTTGGTTATTAACGCAA 	ATGCATCAGGTGATAGTACAGAAGTGAATGCAGTCAACC 	CTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGAT" 	ATATCATTTCGAAAGATGGTAGAAACACTGTGCGCTTA. 	AATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTA 	AAAAAGTAAAAGATTTATCTGATGAAGAAAGAAAGA 	521 GCTGTACGTTTTGTTGACCAAATAATACAATTACAGTCAATACACAAAATGAATTTTTTTT	CCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAG 	GGCGCACGAGTATCTACCAATGTTGCTGACGATGGACAGC 	1. 日本日の出土 くりのじゃ くりの くくりの フロックロック 日本 アコカコ・フェッ
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Qy	oy Db	QY Db	Qy Db	Oy Db	Qy	QY	y d	1 & d	Qy	Oy Db	oy d	l & d	y d	2	QY	Qy Ob	

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HMW protein; hmw gene; hmwAl; hmwA2; high molecular weight; non-typeable Haemophilus influenzae; NTH1; non-encapsulated; recombinant production; Escherichia col1; antibacterial; vaccine; human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis;
Nucleic acid molecule for producing recombinant high molecular weight
                                                                                                                                                                                                                                                                                 /product= "Haemophilus influenzae strain 12 HMW2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proteins of Haemophilus which are used as a vaccine to provide protection against Haemophilus induced diseases in humans -
                                                                                                                                                          Haemophilus influenzae strain 12 hmw2A gene, SEQ ID NO:70.
                                                                                                                                                                                                                                                      Location/Qualifiers
352..4785
                                                                                                                                                                                                                                                                                               protein"
                                                                                                                                                                                                                                  Haemophilus influenzae strain 12.
                                                                                                   AAA52197 standard; DNA; 4940 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                 Klein MH;
                                                      4921 AACAGGTTATTATTG 4937
                                     4921 AACAGGTTATTATTG 4937
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                                                                                                                                                                                                                                                                                                                                                                   98US-0167568
                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                  detection; diagnosis; ds.
                                                                                                                                                                                                                                                                          /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                               2000-303789/26.
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                                                                                                                                         11-SEP-2000
                                                                                                                                                                                                                                                                                                                                               07-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                 07-0CT-1998;
                                                                                                                                                                                                                                                                                                                             13-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                          08-DEC-1998;
                                                                                                                       AAA52197;
                                                                                  RESULT 3
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The invention relates to the recombinant production of Haemophilus influenzae high molecular weight (HWW) proteins in Escherichia coli. The expression construct used to effect recombinant expression comprises a promoter functional in E. coli (e.g., the T7 promoter) operably linked in a modified humwaBC operon from a non-typeable (non-encapsulated) H. clusters termed humwlaBC and humwaABC. Each humwaBC operon comprises humw, mwB and humwC genes. The humw agnes encode the structural HWMA proteins responsible for post-translational processing and secretion of the HWWA proteins. The modified humwaBC operon used in the expression construct of the invention contains an A gene modified such that it encodes only the cand HWMA. The invention also discloses humw agenes (AAAS175-AS2198) strains Joyc, K1, K21, LCDC2, PWH1, 15 and 12. The nucleic acids and evectors are used for the production of recombinant H, influenzae HWWA critical munner response to provide protection against diseases in Example 16; Fig 29A-N; 307pp; English.

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humans caused by H. influenzae (e.g., otitis media, epiglottitis, pneumonia and tracheobronchitis). The HMW proteins are also useful as antigens in immunosassys for detecting antibodies against Haemophilus, HWW proteins and/or HWW peptides. The nucleotide sequences encoding the mon-typeable strains of Haemophilus via hybridisation reactions. The present sequence represents an hmwA gene from other
                                                                                                                                                                                                                                     61 CACCITITITCCAGICTATAFGCAAATATITAAAAAAATAGTATAAATCGCCATATAA 120
                                                                                                                                                                                                                                                                                   121 AATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATCTTTCATCTTTCATCTTTCAT 180
                                                                                                                                                                                                                                                                                                                                                                    240
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                                                                                                                                       99.7%; Score 4924; DB 21; Length 4940; 99.9%; Pred. No. 0; Live 0; Mismatches 0; Indels 3;
                                                                                                            Sequence 4940 BP; 1729 A; 948 C; 1011 G; 1252 T; 0 other;
                                                                                                                                                           Matches 4937; Conservative
                                                                                                                                     Query Match
Best Local Similarity
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Dp	981 GGAA	ATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAATATTACGCTTGAT 204
Οy	2038 CAGG	GTTTTTAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCA 20
Dp	- Q	GTTTTTTAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCA 210
o d	2098 CGCGA	ACCGCGCAAATGCTAAAATTGTCGCCCAGGGCACTGTAACCATTACAGGAGAGGA 215
3 8	158	ATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAAGGTCTGAATATCAT
qq	$\vdash$	
δλ	18 TC	CAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATA 2
qq	2221 TCAT	CAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATA 228
δy	2278 ACAP	ACGAGAAAGAACCTCGTATTGGCAAACCAGCCATGATTCGCAC 23:
qq	2281 ACAP	ACCAAACTACGAGAAAGAACACCTCGTATTGGCAAACCAGCCATGATTCGCAC 234
Qy	338 TGG	
Op	341 TGG	SGTCAGIGCICITAAICIAGAGACAGGCGCAAAITITACCITIAITAAAIACAII 240
QY	398 TC	TAGAAGCTCTGCAGGGTGAATTTTAAC 245
QQ	U	SAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAAC 240
δλ	2458 GGC	AAGAAGGAGCGAAAGTTAATTTCAAATTA 251
qq	- B	taaniggcaacatgtcattcaatctcaaagaaggggggaaagttaatttcaaatta 252
QY	2518 AAAC	CAAACGAGAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATC 257
qq	2521 AAA	CAAACGAGAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATC 258
οy	2578 ACAGC	SACTGGTGGGGGCTCTGTTTTTTGATATATATGCCAACCATTCTGGCAGAGGG 263
qq	2581 ACA	SACTIGITGGGGGCTCTGTTTTTTTTTATATATGCCAACCATTCTGGCAGAGGG 264
δy	: :	3AGTTAAAAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCC 269
QQ	2641 GCT	3AGTTAAAAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCC 270
οy	2698 CAT	STTCGCGGCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAAT 275
QQ	2701 CAT	STICGCGGCGAIGACGCITITAAATCAACAAAGACITAACCATAAATGCAACCAAT 276
Qy	2758 TCA	TCAGCCTCAGACAGACGAAAGATGATTTTATGACGGGTACGCACGC
qq	-0	SAGACAGACGAAAGATGATTTTTATGACGGTACGCACGCAATGCC 282
Qy	2818 ATC	rcaacctacaacatatccattctgggcggtaatgtcacccttggtggacaaaac 287°
qu	2821 ATC	AATICAACCIACAACATAICCATICIGGGGGGTAATGTCACCCTTGGTGGACAAAAC 288
QY	2878 TCA	93
qq	2881 TCA	SAGCAGCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAA 294
ΟŸ	2938 GCC	66
QΩ	- 0	AACGCCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTG 300
Qy	5=	0
QQ	3001 CTC	GTTAATGGGAGTTTAAGTTTAACTGGCGAAAATGCAGATATTAAAGGCAATCTCAC

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4198 AGCATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGC 4257
                                                                             4258 TCGGATATTAAAGCAACCAGCGCACCTTGGTTATTAACGCAAAAGATGCTAAGCTAAAT 4317
                                                                                         4318 GGTGATGCATCAGGTGATAGTACAGAAGTGAATGCAGTCAACGCAAGGGGGTTGTAGT 4377
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                                                                                                                                                                                                                                                                                                                                                           4621 AGTGCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTT 4680
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                                                                                                                                                                    4378 GTGACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGG
                                                                                                                                                                                                                                                                                                      4558 CTTGAAAAGTAAAAGATTTATCTGATGAAGAAAGAGAAACATTAGCTAAACTTGGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                        4798 AAGGTAGATTTCATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTACTGTGTGGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High molecular weight protein; HMW2; protective vaccine; otitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus high molecular weight protein HMW2 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ72294 standard; DNA; 4937 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4918 TTTAACAGGTTATTATTATG 4937
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CAATCTGTTTTAGCAAGCGGCTTACAAGGAATGGATGTAGTACACGGCACAGCCACTATG 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATCTTTCATCTTTCAT 180
                                                                                                                                                                                                                                                                                                                     protect against disease caused by non-typeable Haemophilus which are not controlled by H. influenzae type b (Hib.) vaccines. The encoded protein can also be used as a carrier for protective Hib polysaccharide (in a conjugate vaccin against meningitis) or for other antigens, haptens, etc. This DNA sequence is part of a larger sequence encoding a gene cluster for the hmw2 gene (9323 bp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.5%; Score 4913; DB 15; Length 4937; Best Local Similarity 99.7%; Pred. No. 0; Matches 4922; Conservative 0; Mismatches 15; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4937 BP; 1728 A; 949 C; 1008 G; 1252 T; 0 other;
                                                                                                                                                                                                                          New immunogenic high mol. wt. proteins of non typeable Haemophilus - useful in protective vaccines
                                                                                                                                                                                                                                                                        Claim 3; Page 36; 127pp; English.
                               94WO-US02550.
                                                               93US-0038682.
                                                                                                                                           Barenkamp SJ, St GEME JW;
                                                                                               (BARE/) BARENKAMP S J. (SGEM/) ST GEME J W.
                                                                                                                                                                           WPI; 1994-316665/39.
                                                                                                                                                                                            P-PSDB; AAR63506
                               15-MAR-1994;
                                                               6-MAR-1993;
29-SEP-1994.
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1201 GGTAAACTTTCTGCTGATTCTGTAAGCAAAGATAAAAGCGGCAATATTGTTCTTTCCGCC 1260
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721 GTATTCAACCGTGTTACATCTAACCAAATCTCCCAATTAAAAGGGATTTTAGATTCTAAC 780
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681 G	741 C   741 C	801 A   801 A	861 A       861 A	921 A       921 A	981 AA' 	041 G 041 G	01 G 01 G	61 6	21 T	181 AT	41 AAC	01 AG 	61 GT 	21 CC 21 CC	81 GC 81 GC	41 GA 	01 GTT       01 GTT	61 AA 
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qq	oy P	oy B	QY Dp	oy ob	oy B	Oy Op	Qy Db	Oy Dp	oy G	OY Db	Qy Db	Qy Gb	Qy Db	Oy Db	Qy Db	oy Ob	Qy Dp	δo .

2940 2940 3000 3000 3060 3120 3180 3180 3240 3240 3300 3360 3060 3120 3300 3360 3420 3420 3480 3480 3600 3660 3720 3720 3780 3840 3840 3540 3900 AATICAACCTACAACATATCCATICTGGGCGGTAATGTCACCCTTGGTGGACAAACTCA AGCAGCAGCATTACGGGGAATATTACTATCGAGAAAGCAGCAAAATGTTACGCTAGAAGCC AATAACGCCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC GTTAATGGGAGTTTAAGTTTAACTGGCGAAAATGCAGATATTAAAGGCAATCTCACTATT TCAGAAAGCGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTTT **ACCAATAATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTT ACCAATGATGGTGATTTAAACATTACCACTCACGCTAAACGCAACCAAAGAAGCATCATC** GAAATCCAAATTGGCGGCAATATCTCGCAAAAAGAAGGCAACCTCACGATTTCTTCCGAT GACCTAAGTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTA GACCTAAGTATTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTA AAAAATTAATATCACCAAACAGATAACAATCAAAAAGGGTATTGATGGAGGACTCTAGT ACTATTGGCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCCAAAACAGTAACTTTTAAC **ACCGCGTCGGAAAAGGTTACCACCACAGGCTCGACCATTAACGCAACAAAA** AAAACATCTAGCAGCAATGGCGGACGTGAAAGCAATAGCGACAACGATACCGGCTTAACT **ATTACTGCAAAAAATGTAGAAGTAAACAAAGATATTACTTCTCTCAAAACAGTAAATATC** AATGTTAAAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTG 2821 2821 2881 2881 2941 2941 3001 3061 3121 3001 3061 3121 3241 3241 3361 3361 3541 3661 3181 3301 3301 3421 3481 3481 3541 3601 3601 3421 3721 3781 Op ò ò QQ à q δ qq pp qq ò ò δý QQ qq Db ò ò δλ qq οχ g δy Dp òγ Op gΩ οy à qq οŽ g qq 엄 ò à

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4861 GTTCAGTACGGGCTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTTT 4920
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3901 GITAGCGCGACTGGTGATITAACCACTAAATCCGGCTCAAAAATTGAAGCGAAATCGGGT 3960
         3961 GAGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGGTA 4020
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                                                                                                                                                                                                                                          /*tag= b
/note= "one of a gene cluster for High molecular"
weight protein 2"
7149..9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.8%; Score 4828.2; DB 14; Length 9323; Best Local Similarity 98.6%; Pred. No. 0; Matches 4869; Conservative 0; Mismatches 68; Indels 0; G
                                                                                                                                                                                                                                                                                                   /note= "One of a gene cluster for High molecular"
weight protein 2"
                                                                                                                HMW; high molecular weight protein; virus; vaccine; influenza; epitope; immunity; haemophilus influenzae; gene cluster; ss.
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                                                                                                                                                                                                                  "High molecular weight protein 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High molecular weight surface proteins – of non-typeable haemophilus which exhibit immunogenic properties
                                                                                          Gene cluster for high molecular weight protein 2 (HMW2).
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(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
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                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetic or recombinant vaccines.
                   AAQ49509 standard; DNA; 9323 BP.
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                                                                                                                                                       Haemophilus influenzae.
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Oy Db	801 421 861	ATATATCGTCTCAAATTCAGCAAACGCCTGAATGCTTTGGTTGCTGTGTGTG
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Qy	541	CAATCTGTTTTAGCAAGCGGCTTACAAGGAATGGATGTAGTACAGGGCACGGCACTATG 600 
Qy Dp	601	CAAGTAGATGGTAATAAAACCATTATCGCAACAGTGTTGACGCTATCATTAATTGGAAA 660 
oy Op	661	CAATTTAACATCGACCAAAATGAAATGGTGCAGTTTTTACAAGAAAACAACAACTCCGCC 720 
O <sub>Y</sub>	721	
Qy Db	781	GGACAAGTCTTTTAATCAACCCAAATGGTATCACAATAGGTAAAGACGCAATTATTAAC 840 
Qy Db	841	AGGCGCGTAAT 90.                      AGGCGCGTAAT 13.
Qy Db	901	
O.Y Db	961	ACTGTCGGTAAAGACGCAGTGTAAATCTTATTGGTGGCAAAGTGAAAAACGAGGGTGT 1020 
Oy Db	1021	ATCACCATCAGCGAT 1080
Oy Dp	1081	GCGGTCAATCTG 114 
Oy Ob	1141	GGCGATATTTTGCCAAAGGCGGTAACATTAATGTCCGTGCTGCCGCTATTCGAAACCAA 1200 
2y ob	1201	PATGTTCTTTCGCC 126

1380 1500 2000 1620 2060 1680 2120 1741 CCAACAGGCACGGTGAAGCAAGCGACCCTAAAAAATAGCGAACTCAAAACAACGCTA 1800 1860 2300 1920 2360 1980 2420 2040 2480 2100 GACGCGCCAAATGCTAAAATTGTCGCCCAGGGCACTGTAACCATTACAGGAGGGAAAA 2160 2541 GACGCGCAAATGCTAAAATTGTCGCCCAGGCACTGTAAACCATTACAGGAGAAAA 2600 GATTICAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 2220 2340 2341 AACGICAGIGCICTTAAAICTAGAGACAGGCGCAAATITIAACCTITAATAAAIACAITICA 2400 GGCAAGCTGATGATTACAGGGGATAAAGTCACATTAAAAACAGGTGCAGTTATCGACCTT GGCATTCAATTAGCAAAGAAAACCTCTTTAGAAAAAGGCTCAACCATCAATGTATCAGGC 1501 AAAGAAAAAGGGGGACGGGTATTGTGGGGGGGGATATTGCGTTAATTGACGGCAATATT 2001 AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGGAGACACTCGGGCAT AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGGAGACATCGGGGGAT TATTTATCCATTGACAGCAATGCAATTGTTAAAACAAAAGAGTGGTTGCTAGACCCTGAT ACCAATACAACTATTTCAAATTATCTGAAAAACGCCTGGACAATGAATATAACGGCATCA 1861 AGAAAACTTACCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATTCTCCAT 1981 AATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG GGTTTTTTAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 2281 ATTAACCAAACTACGAGAAAGAACACCTCGTATTGGCAAACCAGCCATGATTCGCACTGG 1321 1381 1441 1561 1621 2061 1801 2041 2101 2161 2601 2721 q ò q qq ó δ q ò qq QQ ò δ g ò g ò g ò Ω ŏ qq ò qq Q δ δy g οy Q ò Q ò qq αq ò

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Dp	Qy	Qy	Qy Dp	QY Dp	Qy Db	Qy Db	ç D	oy ob	δ O	Qy Db	Qy Db	Qy Dp	Qy Dp	Qy Db	QY	QY Db	QY	QY

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## ## ## ## ## ## ## ## ## ## ## ## ##		21 ACCGCGTCGGAAAGGTTACCACCACAGGGGCTCGACCATTAACGCAACAAATGGCAAAA  41 GCAAGTATTACAACCCAAAACGGGATATCAGGGGTACGATTAACGGGAACAAAGTGGCAAA  52 GCAAGTATTACAACCAAAACAGGTGATATCAGCGGTACGATTTCCGGTAACAGGTAAGT  63 GTTAGCGGACTGGTGATTTAACACACTAAATCCGGTCCAAAAATTGAAGCGAAATCGGGGT  64 GTTAGCCGACTGGTGATTTAACACACTAAATCCGGCTCAAAAATTGAAGCGAAATCGGGG  65 GTTAGCCGACTGGTGATTTAACACACTAAATCCGGCTCCAAAAATTGAAGCGAAATCGGGG  66 GTTAGCCGACTGGTGATTTAACACACTAAATCCGGCTCCAAAAATTGAAGCGAAATCGGGT  67 GTTAGCCGGACTGGTGATTTAACCACTAAATCCGGCTCCAAAAATTGAAGCGAAATCGGGT  67 GTTAGCCGGACTGGTGATTTAACCACTAAATCCGGCTCCAAAAATTGAAGCGAAATCGGGTAAATCCGGCTAAAAACCGGCTAAATCCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAAACCGGCTAAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAAACCGGCTAAAAACCGGCTAAAAACCGGCTAAAAACCAAAAAACCAAAAAACCAAAAAAACCAAAAAA	61 GAGGCTAATGCTAACAGGGTAAATGCGGGTAACAGGGTAATGCGGAAATGCTTAGGGGAAACGGTATTAAGGGGAATGCTTAGGGGAAATGCTTAAGGGGAAATGATTAATGCGAAATGATTAGGGGAATGCTTAGGCGAAATTAATGCGGAAATGATTAATGCGGAAATGATTAATGCGGAAATGATTAATGCGGAAATGATTAATGCGGAAATGATTAATGCGGAAATGATTAAGCGGGAATGATTAATGCGGAAATGATTAATGCGGAAATGATTAATGCGGAAATGATTAATGCGGAAATGATTAATGCGGAAATGATTAATGCGGAAATGATTAATGAGCGGGAATTAATGAGCGGGAATGATTAATGAGCGGGAATAATGATTAAGCGGGAATAACTTAAGCGGGAATAATGATTAAGCGGGAATAACTTAAGCGGGAATAACTTAAGCGGGAATAACTTAAGCGGGAATAACTTAAGCGGGAAATAACTTAAGCGGGTAATAAGCGGGAATAACTTAAGCGGGAATAACTTAAGCGGGAATAACTTAAGCGGGTAATAAGCGGGAATAACTTAAACTGAAGCCGGTTATAAGCGGAAATAACTTAAACTGAAGCCGGGTTATAAGCGGAAATAACTTAAACTGAAGCCGGTTATAAGCGGAAATAACTTAAACTGAAGCCGGTTATAAGCGGAAATAACTTAAACTGAAGCCGGTTATAAGCGGAAATAACTTAAACTGAAGCCGGTTAATAAGCGGAAATAACTTAAACTGAAGCCGGTTAAACTAAGCAGGAAATAACTTAAACTAAACTAAACTAAACTAAACTAAACTAAAAATAAAAAA	41 ATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAAGC		
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                            4681 ACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTAAT 4740
                                                                                                           GCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTTACA 4680
                                                                                                                                                                                                                                                                                                                                          4800
                                                                                                                                                                                                                                                                                                                                                                                                                               4801 GTAGATITCATCCIGCAAIGAAGICATITITATITICGIAITATITACIGIGIGGGITAAA 4860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5241 GTAGATTTCATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTACTGTGTGGGGTTAAA 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCAGTACGGGCTTTACCCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTTT 4920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAAAAGTAAAAGATTTATCTGATGAAGAAAGAGAAACATTAGCTAAACTTGGTGTAAGT
                                                                                                                                 GGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACAAG
                                                                                                                                                                                                                                                                                                                                                     Non-typeable Haemophilus; high molecular weight surface protein;
HMW2; hmw2 gene; immunogen; vaccine; otitis media; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              High molecular weight proteins of non-typeable Haemophilus
influenzae – useful for vaccine production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Non-typeable Haemophilus influenzae hmw2 gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
792..5222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/note= "hmw2 gene"
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/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae strain 12.
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/note= "ORF-c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5361 AACAGGTTATTATTATG 5377
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This nucleic acid comprises a gene cluster for the hmw2 gene (see also AAT90995) that encodes high molecular weight surface protein HMM2 (see AAM30294) of non-typeable Haemophilus influenzae strain 12. In addition to the hmw2 gene there are 2 additional downstream open reading frames that are required for the correct processing and secretion of the hmw1 gene product. The ORF-b derived amino acid sequence demonstrates similarity with the derived amino acid sequences of 2 genes which encode proteins required for secretion and activation of haemolysins of P. mirabilis and S. marcescens. HWM proteins (see AAW30291-94) can be used in vaccines, as Immunogens for preparation of antibodies and as antigens for detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 CACCTTTTTGCAGTCTATATGCAAATATTTTAAAAAATAGTATAAATCCGCCATATAA 120
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tive 0; Mismatches
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781 GGACAAGTCTTTTAA 1221 GGACAAGTCTTTTAA 1221 GGACAAGTCTTTTTAA 1281 ACTAATGGCTTTACG 1281 ACTAATGGCTTTACG 1281 ACTAATGGCTTAACG 1281 ACTAATGGCTAAAGAC 1401 ACTGTCGGTAAAGAC 1021 ATTACCGTAAAAGAC 1021 ATTACCGTAAAAGAC 1021 ATTACCGTAAAAGAC 1021 ATTACCGTAAAAAGCC 1201 GGTAAACTTTTCCC 1201 GGTAAACTTTTCCC 1201 GGTAAACTTTTCCC 1201 GGTAAACTTTTCCC 1201 GGTAAACTTTCTCCT 1201 GGTAAACTTTTTGCC 1201 AAAGAGGGTGAAGCG 1321 GGCAAGCTGATGATT 1111111111111111111111111111111	TCAACCCAAATGGTATCACAATAGGTAAAGACGCAATTATTAAC 840		TAGACATTANTGCCGTGGTGCCACTATTCGAAACAA 120 AAAACATTAATGTCCGTGGTGCCACTATTCGAAACAA 120 SGTAACATTAATGTCCGTGGTGCCACTATTCGAAACAA 120 SGTAACATTAATGTCCGTGGTGCCACTATTCGAAACAA 120 STAAGCAAAAAAAAAAGCGGCAATATTGTTCTTTCCGCC 126 STAAGCAAAAAAAAGCGGCAATATTGTTTTCTTCCGCC 170	GAAATTGGCGGTGTAATTTCCGCTCAAAATCAGCAAGCTAAAGGC 1320	AAGAAAACCTCTTTAGAAAAGGCTCAACCATCAATGTATCAGGC 1500	In
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	78 22 22 28 34 34	96: 140: 102: 146:	134. 114. 158. 120.	126 170 132 176 138 182	144 188 150 194 156	62. 06. 12. 18. 18. 24.

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AATTCTCC              AATTCTCC	TAAAGGCG           TAAAGGCG	GCTTGATC	CAAAGCAC	AGAGGGAA              AGAGGGAA	TATCATTT	GAATATAA               GAATATAA	VITCGCACT	AATACATTI            AATACATTI	ATTTTAACG	CAAATTAA 	CCAATATCA 	SCAGAGGG             SCAGAGGGG	TAAATTCCC           TAAATTCCC	CAACCAAT! 	GCAATGCC,	GACAAAAC' 	CGCTAGAA	GCAGCTTG
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861 AGAAAACTTACCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATTCTCCAT 1920 	rgatggaga                 rgatggaga	FGTTCATAA                FGTTCATAA	rtttgaagg                tttgaagg	CACTGTAAC 	AACGGGTAA              AACGGGTAA	CACAATTAA [111111] CACAATTAA	TTGGCAAAC             TTGGCAAAC	AAATTTTAC 	AAGCTCTGC 	AGGAGCGA/              AGGAGCGA/	ACCAATTCC 	ATATGCCA            ATATGCCA	CGGCGCTA	AGACTTAA              AGACTTAA	TTATGACG	STAATGTCA 	AGAAAGCAG	GGATAGAGTTATAAAACTTGGCAGCTTGCTC
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AATAGCTCA 	GCGGAGGC              GCGGAGGC	rcregegga              rcregegga	ACCGCCGCT 	AAAATTGTC               AAAATTGTC	AACGTATCT	ACCCACAAT             ACCCACAAT	AGAAAGAAC                AGAAAGAAC	AATCTAGAC	TTAACAACA 	TCATTCAAT	AACACAAGG	TCTGTTTT 	GAAATTAA 	GCTTTTAA 	ACAGACGAA                ACAGACGAA	CATATCCAT	GGGAATAT	AGCAGCCCTAATCAGCAAAACATAAG
TTACCGTT	GTCAGCGTC             GTCAGCGTC	CCATTTAT	TAAATATT             TAAATATT	CAAATGCT	GGGCTAAC.	ATAATTA            ATAATTTA	AAACTACG	AGTGCTCTT	AGCAAAGGC            AGCAAAGGC	GCAACATG 	SAGAACATG 	3GTGGGGGG            3GTGGGGGG	AAAATGAGT              AAAATGAGT	GGCGATGAC            GGCGATGAC	AGCCTCAGA 	ACCTACAAC 	AGCATTACC	GCCCCTAA
AGAAAAC              AGAAAAC	AGTAAAG          AGTAAAG	AATTTAA          AATTTAA	GGTTTT          GGTTTT	GACGCGG          GACGCGG	GATTTCA          GATTTCA	TCAGTGA         TCAGTGA	ATTAACO	AACGTCA               AACGTCA	AGCAATA             AGCAATA	GTAAATC         GTAAATC	CCAAACC        CCAAACC	GCCACTO         GCCACTO	GAGTTA       GAGTTA	GTTCGC         GTTCGC	AATTTC          AATTTC	AATTCA          AATTCA	AGCAGC	AGCAGC
1861	1921	1981	2041	2101	2161	2221	2281	2341	2401	2461	2521	3021	2641	3141	2761 3201	2821	2881	2941
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DNA encoding Haemophilus influenzae strain 12 mature hmw2A, SEQ ID NO:72.
4461 AATGTTACGGCAAACGCTGGCGATTTAACAGTTGGGAATGGCGCAGAAATTAATGCGACA 4520
                      GAAGGAGCTGCAACCTTAACCGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCTAGC 4140
                                 4141 ATCACTICAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAAGC 4200
                                                                          ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGCTCG 4260
                                                                                                                    4261 GATATTAAAGCAACCAGCGGCACCTTGGTTATTAACGCAAAAGATGCTAAGOTAAATGGT 4320
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Mature HWW protein; hmw gene; hmwAl; hmwA2; high molecular weight; non-typeable Haemophilus influenzae; NTHi; non-encapsulated; recombinant production; Escherichia coll; antibacterial; vaccine; human disease; ottitis media; epiglottitis; pneumonia; tracheobronchitis; detection; diagnosis; ds.

Haemophilus influenzae strain 12.

Location/Qualifiers 1675..4782 /\*tag= a mat\_peptide

/\*tag= a /product= "Haemophilus influenzae strain 12 mature HMW2A protein"

WO200020609-A2.

13-APR-2000.

99WO-CA00938. 07-OCT-1999; 98US-0167568. 98US-0206942. 07-OCT-1998;

(CONN-) CONNAUGHT LAB LTD.

Loosmore SM, Yang Y, Klein MH;

WPI; 2000-303789/26. P-PSDB; AAB01849 Nucleic acid molecule for producing recombinant high molecular weight proteins of Haemophilus which are used as a vaccine to provide protection against Haemophilus induced diseases in humans

Claim 7; Fig 29E-N; 307pp; English.

The invention relates to the recombinant production of Haemophilus

Influenzae high molecular weight (HMW) proteins in Escherichia coll. The
expression construct used to effect recombinant expression comprises a
promoter functional in E. coli (e.g., the T7 promoter) operably linked

to a modified hwwABC operon from a non-typeable (non-encapsulated) H.

Influenzae (NTHI). Most HMW-expressing NTHI strains contain two hmw gene
clusters termed hmwABC. Each hmwABC operon comprises hmwA,
clusters termed hmwABC. Each hmwABC operon comprises hmwA,
clusters termed hmwABC and hmwABC. Each hmwABC operon comprises hmwA,
and the hmwB and hmwC genes encode accessory proteins which are
responsible for post-translational processing and secretion of the HMWA
contains and sand a gene modified such that it encodes only the
mature HMWA. The invention also discloses hmwA genes (AAASI199)
mature HMWA proteins (AAB01824-801849) from the non-typeable H. Influenzae
and HMWA proteins (AAB01824-801849) from the non-typeable H. Influenzae
strains Joyc, KI, K21, LCDC2, PMHI, 15 and 12. The nucleic acids and
proteins which can be used as vaccines to mediate a humoral or
cell-mediated immune response to provide protection against diseases in
humans caused by H. Influenzae (e.g., otitis media, epiglottitis,
humans caused by H. Influenzae (e.g., otitis media, epiglottitis,
endiates and cracheobronchitis). The HMW proteins are also useful as
antiquens in immunoassays for detecting antibodies against Hemophilus,
HWW proteins and/or HWW peptides. The nucleotide sequences encoding a mature
converged to the protein and classified of the modified NTHI hmwA gene encoding a mature
converged to the proteins and of the modified NTHI hmwA gene encoding a mature
converged to the proteins and modified of HWA proteins.

Sequence 3263 BP; 1173 A; 628 C; 674 G; 788 T; 0 other;

Gaps ; DB 21; Length 3263; 0; Indels ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Score 3263; Pred. No. 0 66.1%; Similarity Matches 3263; Ouery Match

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1675 CCTGATGATGTAACAATTGAAGCCGAAGACCCCCTTCGCAATAATACCGGTATAAATGAT 1734 ŏ g

2815 GCCATCAATTCAACCTACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAA 2874 2395 ATTICAAGCAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTT 2454 2515 TTAAAACCAAACGAGAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAAT 2574 2635 GGGCCTGAGTTAAAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTÄCTTAAAT 2694 2155 GGAAAAGATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATC 2214 2275 ATAACAATTAACCAAACTACGAGAAAGAACACCTCGTATTGGCAAACCAGCCATGATTCG 2334 2335 CACTGGAACGTCCAGTGCTCTTAATCTAGAGACAGGCGCAAATTTTACCTTTATTAAATAC 2394 GATCAGGGITTTTTAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAA 2094 1855 GCATCAAGAAAACTTACCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATT 1914 1915 CICCATAGTAAAGGTCAGCGTGGCGGAGGCGTTCAGATTGATGGAGATATTACTTCTAAA 1974 1975 GCCGGAAATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTT 2034 2095 GCACGCGACGAGCAAATGCTAAAATTGTCGCCCAGGGCACTGTAACCATTACAGGAGAG 2154 241 CTCCATAGTAAAGGTCAGCGTGGCGGAGGCGTTCAGATTGATGGAGATATTACTTCTAAA 300 2035 οy g Dβ pp οy g δ q δy Dp δ qq δλ qq Op ò QQ δ QQ QY qq рþ δ Ω d δλ a óλ рp ά g ò g δ δy

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1141 G	2875 A       1201 A	2935 G	2995 T	3055 AC 1381 AC	3115 AZ       1441 AZ	3175 AA     1501 AA	3235 AT      1561 AT	3295 GA      1621 GA	3355 TC    1681 TC	3415 TC     1741 TC	3475 AC    1801 AC	3535 GA    1861 GA	3595 TT    1921 TT	3655 AA.    1981 AA.	3715 TT	3775 AAC 11 2101 AAC	3835 GGC       2161 GGC	3895 GTA
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2221 GTAAGTGTTAGCGCGACTGGTGATTTAACCACTAAATCGGGCTCAAAAATTGAAGCGAAA 2280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 ATGACAAACAACTATACAACACCTTTTTTGCAGTCTATATGCAAATATTTTAAAAAAT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 AGTATAAATCCGCCATATAAAATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.3%; Score 2680.2; DB 14; Length 5116; 73.5%; Pred. No. 0; tive 0; Mismatches 1093; Indels 265; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The isolation and purification of the high molecular weight protein enables the identification of the major protective epitopes of the protein by conventional epitope mapping. These epitopes can then be synthesised using standard techniques and incorporated into fully
                                                                                  HMW; high molecular weight protein; virus; vaccine; influenza; epitope; immunity; haemophilus influenzae; ss.
                                                                                                                                                                                                                                                                /*tag= d
/transl_except= AAG encodes Asparagine.
misc_difference 1674...1676
/*tag= e
/transl_except= CCG encodes Phenylalanine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5116 BP; 1766 A; 1008 C; 1037 G; 1305 T; 0 other;
                                                                                                                                                                 /*tag= a //rage a //rage a //rage //rage a //rage //rage a //rage 360..362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High molecular weight surface proteins - of non-typeable haemophilus which exhibit immunogenic properties
                                                              Sequence encoding high molecular weight protein 1 (HMW1).
                                                                                                                                                                                             /*tag= b//translexcept= CTA encodes Isoleucine.misc_difference 642..644
                                                                                                                                                                                                                          /*tag= c
/transl_except= GAU encodes Alanine.
misc_difference 1437..1439
                                                                                                                                                                                                                                                                                                                                                                                                                    (BARE/) BARENKAMP S J.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic or recombinant vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Figure 1; 100pp; English.
AAQ49506 standard; DNA; 5116 BP
                                                                                                                                                                                                                                                                                                                                                                                              92GB-0005704.
                                                                                                                                                                                                                                                                                                                                                                         93WO-US02166
                                         26-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 3761; Conservative
                                                                                                                                                    ..4961
                                                                                                                                                    351..496
/*tag=
                                                                                                                    Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-320683/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR41723
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barenkamp SJ;
                                                                                                                                                                                                                                                                                                                                                                           16-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                               16-MAR-1992;
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                     AAQ49506;
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1001 AAGTGAAAAACGAGGGTGTGATTAGCGTAAATGGTGGCAGCATTTCTTTACTCGCAGGGC 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1181 CTGCCACTATTCGAAACCAAGGTAAACTTTCTGCTGATTCTGTAAGCAAAGATAAAAGCG 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1241 GCAATATIGITCTTTCCGCCAAAGAGGGTGAAGCGGAAATIGGCGGTGTAATTTCCGCTC 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              941 TIGIGAAICACGGITIAATIACIGICGCIAAAGACGGCAGIGIAAAICTIAITGGIGGCA 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        641 ACGCTATCATTAATTCGAAACAATTAACATCGACCAAAATGAAATGGAAGTGCCGTTTTTAC 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        701 AAGAAAACAACAACTCCGCCGTATTCAACCGTGTTACATCTAACCAAATCTGCCAATTAA 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          761 AAGGGATTTTAGATTCTAACGGACAAGTCTTTTTAATCAACCCAAATGGTATCACAATAG 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     821 GTAAAGACGCAATTATTAACACTAATGGCTTTAACGGCTTCTACGCTAGACATTTCTAACG 880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400 TTGCTGTGTCTGAATTGGCACGGGGTTGTGACCATTCCACAGAAAAAGGCAGCAAAAAAC 459
                                                                                                                                                                                                                                                                                461 TIACTATCTTAGGTGTAACCACTTAGGGTTAAAGCCACTTTCCGCTATGTTACTATCTT 520
                         281 GAATGAAGAGGGAGCTGAACGAACGCAAATGATAAAGTAATTTAATTGTTCAACTAACCT 340
                                                                                                        341 TAGGAGAAAATATGAACAAGATATATCGTCTCAAATTCAGCAAACGCCTGAATGCTTTGG 400
                                                                                                                                                                                                                    401 TIGCIGICTCTGAATIGGCACGGGGTTGTGACCATICCACAGAAAAAGGCTICCGCTAIG 460
160 TITCATCTITCATCTITCATCTITCATCTITCATCTITCATCTITTCATCTTTCATCTTTC 219
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Oy Dp	1301	AAAATCAGCAAGCTAAAGGCGGCAAGCTGATGATTACAGGCGATAAAGTCACATTAAAA 1360 
Q Dp	1361	CAGGTOCAGTTATCGACCTTTCAGGTAAAGAGGGGAGAAACTTACCTTGGCGGTGACG 1420 
Oy Dp	1421	AGCGCGCGCGAAGGTAAAAACGGCATTCAATTAGCAAAGAAAACCTCTTTAGAAAAGGCT 1480 
oy Oy	1481	CAACCATCAATGTATCAGGCAAAGAAAAAGGCGGACGCGCTATTGTGTGGGGGCGATATTG 1540 
δy	1541	SCTAAAACCGGTGGTT 1
λο a	1601	3TTAAAACAAAAG 166               3TTGACGCCAAAG 165
Qy Dp	1661 1660	A 172
Qy	1721	4 8
S G	1781 1780	A 184 I 183
λ O O	1841	CAATGAATATAACGGCATCAAGAAAACTTACCGTTAATAGCTCAATCAA
λ α	1901	ATAGTAAAGGTCAGCGTGGCGGAGGCGTTCAGA 
λς Op	1961 1954	3 200 1 3 201
ζ	2009	GGCTTGATCAGGGTTTTTTAAATATTACCGCGCGCTTCG 206: 
λζ QC	2069	TAGCTITIGAAGGIGGAAATAACAAAGCACGGACGGCGAAATGCTAAAATTGTCGCC 2128 
λ q	2129	NCAACGFATCTTTAA 218 
<b>≿</b> 9	2189	ACGGAACGGGTAAAGGTCTGAATATCATTTCATCAGTGAATAATTTAACC 2239 
ξ, q	2240	ACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACAATTAACCAAACTACGA 2296 
≿ <b>9</b>	2297	CGTCAGTGCTCTTA 235 

2357 ATCT---AGAGACAGGCGCAAATTTTACCTTTAATTAAATACATTTCAAGCAATAGCAAAG 2413 2356 ATGTTTCCGAGAGGGGGAGTTTAACCTCACTATTGACTCCAGAGGAGGGATAGTGCAG 2415 2414 GCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGCGTAAATGGCAACA 2473 2416 GCACACTTACCCAGCCTTATAATTTAAACGGTATATCATTCAACAAAGACACT---ACCT 2472 2474 IGTCATTCAATCTCAAAGAAGGAGCGAAAGTTAATTTCAAATTAAAACCAAACGAGAACA 2533 2473 TTAATGTTGAACGAAATGCAAGAGTCAACTTTGACATCAAGGCACCAATAGGGATAAATA 2532 2534 TGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACAGCCACTGGTGGGG 2593 2533 AGTATTCTAGTTTGAATTACGCATCATTTAATGGAAACATTTCAGTTTCGGGAGGGGGGA 2592 2594 GCTCTGTTT-----TTTTTGATATATATGCCAACCATTCTGGCAGGGGGCCTGAGTTAA 2647 2713 CABARACTGGCTTCTCAATAGAGAAAGATTTAACTTTAAATGCCACC-----GGAGGCA 2766 2593 GIGITGATITCACACTICTCGCCTCATCCTAACGTCCAAACCCCCGGTGTAGTTATAA 2652 2648 AAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCCCATGTTCGCG 2707 2708 GCGATGACGCTTTTAAAATCAACAAGACTTAACCATAAATGCAACCAATTCAAATTTCA 2767 2767 ACATAACACTITIGCAAGITGAAGGCACCGAIGGAATGAITGGIAAAGGCAITGIAGCCA 2826 2947 TTGACAACCATCAAAA-----ACCTTTAACTATTAAAAAAGTGTCATCATTAATAGCG 3000 2828 CCTACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCAAGCAGCA 2887 2888 GCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCCAATAACG 2947 3001 GCAACCTTACCGCTGGAGGCAATATTGTCAATATAGCCGGAAATCTTACCGTTGAAAGTA 3060 2827 AAAAAAACATAACCTTTGAAGGAGGTAACATCACCTTTGGCTCCAGGAAAGCCGTAACAG 2886 2948 CCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTCGTTAATG 3007 3008 GGAGTTTAAGTTTAACTGGGGAAAATGCAGATATTAAAGGCAATCTCACTATTTCAGAAA 3067 3068 GCGCCACTITTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTITACCAATA 3127 3061 ACGCTAATTTCAAAGCTATCACAAATTTCACTTTTAATGTAGGCGGCTTGTTTGACAACA 3120 3121 AAGGCAATTCAAATATTCCATTGCCAAAGGGGGGTCGCTTTAAAGACATTGATAATT 3180 3181 CCAAGAATTTAAGCATCACCACCAGCTCCACTTACCGCACTATATAAGCGGCA 3240 3128 ATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTTACCAATG 3187 3188 AIGGIGATITAAACATTACCACTCACGCTAAACGCAACCAAAGAAGCATCATCGGCGGAG 3247 3248 ATATAATCAACAAAAAGGAAGCTTAAATATTACAGACAGTAATAATGATGCTGAAATCC 3307 3308 AAATTGGCGGCAATATCTCGCAAAAAGAAGGCAACCTCACGATTTCTTCCGATAAAATTA 3367 3301 AAATTGGCGGCGATGTCTCGCAAAAAGAAGGTAATCTCACGATTTCTTCTGACAAAATCA 3360 3368 ATATCACCAAACAGATAACAATCAAAAGGGTATTGATGGAGAGAGCTCTAGTTCAGATG 3427 3428 CGACAAGTAATGCCAACCTAACTATTAAAACCAAAGAATTGAAATTGACAGAAGACCTAA 3487 g δ g ò g ð 원 οy g ò g ŏ g δ g g ò g ò g ŏ δ g q ŏ Q a ŏ

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4978 AGGIAGATITCAICCTGCAATGAAGICAITTTATTITCGTAITAITTACTGTGTGGGTTA 5037
                                                                                                                                                                                                                                                                                                                                                                                                 4859 AAGTTCAGTACGGGCTTTACCCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATT 4918
                                                                                                                                                            4559 TIGAAAAAGIAAAAGAITIAICIGAIGAAGAAAAGAAAACAITAGCIAAACIIGGIGIAA 4618
                                                                                                                                                                                                         4619 GIGCTGTACGTTITGTIGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTTA 4678
                                                                                                                                                                                                                                                                  4739 ATGGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACA 4798
                                                                                                                                                                                                                                                                                                                         4918 ATGGCGCGACGGTGTGCGTTAATATCGCTGATAACGGGCGGTAGCGGTCAGTAATTGACA 4977
                                                                                 4499 TGAAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCC 4558
                                                                                                                             4679 CAACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTA 4738
                      4379 TGACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGT 4438
                                 4439 TAAATATCATTTCGAAAGATGGTAGAAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGG 4498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High molecular weight protein; HMW1; protective vaccine; otitis; sinusitis; bronchitis; Hib; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haemophilus high molecular weight protein HMW1 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ72293 standard; DNA; 5116 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           5098 TTAACAGGTTATTATTATG 5116
                                                                                                                                                                                                                                                                                                                                                                                                                                                4919 TTAACAGGTTATTATG 4937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94WO-US02550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barenkamp SJ, St GEME JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BARE/) BARENKAMP S J. (SGEM/) ST GEME J W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-316665/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR63505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ72293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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The HMW1 protein encoded by this sequence is useful in a vaccine to protect against disease caused by non-typeable Haemophilus which are not controlled by H. influenzae type b (Hib) vaccines. The encoded protein can also be used as a carrier for protective Hib polysaccharide (in a conjugate vaccin against meningitis) or for other antigens, haptens, etc. This DNA sequence is part of a larger sequence encoding a gene cluster for the hmw1 gene (9011 bp).
                                                                                                                                                                                                                                                                                                                             Ouery Match

54.3%; Score 2680.2; DB 15; Length 5116;
Best Local Similarity 73.5%; Pred. No. 0;
Matches 3761; Conservative 0; Mismatches 1093; Indels 265;
                                                                                                                                                                                                                                                                                      Sequence 5116 BP; 1766 A; 1008 C; 1037 G; 1305 T; 0 other;
                                non typeable
                   New immunogenic high mol. wt. proteins of m Haemophilus – useful in protective vaccines
                                                                             Claim 2; Page 28; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161
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16; 41 ATGACAAACAATTACAACACCTTTTTTGCAGTCTATATGCAAATATTTTAAAAAAT 100 101 AGTATAAATCCGCCATATAAAATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATC 160 TITCAICITICALCITICATCITICATCITICATCITICATCITICATCITICATCITIC 220 GAATGAAGAGGGAGCTGAACGAACGCAAATGATAAAGTAATTTAATTGTTCAACTAACCT 340 TIGCIGIGICIGAAIIGGCACGGGGIIGIGACCAIICCACAGAAAAAGGCIICCGCIAIG 460 520 700 TAGGTGTAACATCTATTCCACAATCTGTTTTAGCAAGGGGCTTACAAGGAATGGATGTAG 580 579 TACACGGCACAGCCACTATGCAAGTAGATGGTAATAAAACCATTATCCGCAACAGTGTTG 640 Gaps 760 759 TTACTATCTTTAGGTGTAACCACTTAGCGTTAAAGCCACTTTCCGGCTATGTTACTATCTT ACGCTATCATTAATTGGAAACAATTTAACATCGACCAAAATGAAATGGTGCAGTTTTTAC AAGAAAACAACTCCGCCGTATTCAACCGTGTTACATCTAACCAAATCTCCCAATTAA 220 281 280 221 401 161 521 520 581 580 641 640 701 200 g q

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DP QY	820	AAGACGCAATTATTAACACTAATGGCTTTACGGCTTCTACGCTAGACATTTTAACG 8 ACATCAAGGCGTTCAATGGCTTTACGGCTTCTACGTAGACATTAACG 8
οqα		
Qy Dp	941	TTGTGAATCACGGTTTAATTACTGTCGGTAAAGACGGCAGTGTAAATCTTATTGGTGGCA 1000 
Qy	1001	AAGTGAAAAACGAGGGTGTGATTAGGGTAAATGGTGGCAGCATTTCTTTACTCGCAGGC 1060 
Qy Dp	1061	AAAAAATCACCATCAGGGATATAATAAACCCAACCATACTTACAGCATTGCCGCGGCTG 1120 
Oy Dp	1121	AAAATGAAGGGTCAATCTGGGGGGATATTTTGCCAAAGGGGGTAACATTAATGTCCGTG 1180 
QV	1181	AAGATAAAAGCG 1240 
Qy Db	1241	GCAATATTGTTCCGCCAAAGAGGTGAAGCGGAAATTGGCGGTGTAATTTCCGCTC 1300 
Qy	1301	AAAATCAGCAAGCTAAAGGCGGCAAGCTGATGATTACAGGCGATAAAGTCACATTAAAA 1360 
Qy Db	1361 (	
Qy Db	1421 /	
Qy Db	1481 C	FTG 154
Qγ	1541 C	CGTTAATTGACGGCAATATTAACGCTCAAGGTAGTGGTGATATCGCTAAAACGGGGGTT 1600 
Qy	1601 T   1600 T	TTGTGGACACATGGGGGATTATTTATGCATTGACAGCAATGCATTGTTAAAACAAAAG 1660 
Qy Db	1661 A     	GTGGTTGCTAGACCCTGATGAACAATTGAAGCGAAGACCCCCTTGGCAATAATA 172 
Qy Dp	1721 C   1720 C	CGGTATAAATGATGAATTCCCAACAGGCACCGGTGAAGCAAGC
Qy	1781 G 1780 A	CGAACTCAAAACAAGGTAACCAATACAACTATTCAAATTATCTGAAAAAGGCCTGGA 1840 
Qy Db	1841 C	CAATGAATATAACGGCATCAAGAAAACTTACCGTTAATAGCTCAATCAA
ογ	1901 A	CTCCCACTTAATTCTCCATAGTAAAGGTCAGCGGGGGGGG

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qq	1894	ATGGCAGCTTAACTCTTTGGAGTGAGGGTCGGAGCGGTGGCGGCGTTGAGATTAACAACG 1	1953
λa	51	ATATTACTTCTAAAGGCGAAATTTAACCATTTATCTGGCGGATGGG 2   111111   1111	2008
90 0	2009	. (5	2068
; g	2014		2073
Oy Db	2069	TAGCTTTTGAAGGTGGAAATAACAAAGCACGCGCGCGCGAAATGCTAAAATTGTCGCCC 2	2128
Oy Dp	2129	AGGGCACTGTAACCATTACAGGAGAGAGAGATTCAGGGCTAACAACGTATCTTAA 2	188
Qy Dp	2189	ACGGAACGGGTAAAGGTCTGAATATCATTTCATCAGGATAATTTAACCC 2	2239 2235
Oý Dp	2240		2296 2295
oy Op	2297		2356 2355
Qy Dp	2357		2413 2415
Qy Dp	2414	GCTTAACAACAGTATAGAAGCTCTGCAGGGTGAATTTTTAACGGCGTAAATGGCAACA ;	2473
Qy Dp	2474	TGTCATTCAATCTCAAAGAAGAGCGAAAGTTAATTTCAAATTAAAACCAAAGGGAAACA 	2533 2532
Qy Db	2534	TGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACAGCCACTGGTGGGGG	2593 2592
Oy Db	2594	GCTCTGTTTTTTTGATATATGCCAACCATTCTGGCAGAGGGCTGAGTTAA	2647 2652
çy Pp	2648	AAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCCCATGTTCGCG	2707
δ ά	2708	GCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCAAATTTCA	2767
o y	2768	GCCTCAGACGAAAGATGATTTTATGACGGGTACGCACGCA	2827
qq	2767		2826
δō i	2828	CCTACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCAAGCAGCA	2887
Ω	1787		
Oy Dp	2888	GCATTACGGGGATATTACTACGAGAAGCAGGAATGTTACGCTAGAAGCCAATACG 	2946
Qy	2948	CCCCTAATCAGCAAAAC	3007
QQ	2947	TTGACAACCATCAAA	3000

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AAT90994 standard; DNA; 5116 BP.

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                                                                                                                                                                                                                                                                                                                              TAAATATCATTTCGAAAGATGGTAGAAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGG 4498
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Non-typeable Haemophilus; high molecular weight surface protein; HMW1; hmwl gene; immunogen; vaccine; otitis media; ss.
                           Non-typeable Haemophilus high mol.wt. surface protein hmwl gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae strain 12 that encodes high molecular weight surface protein HWMI (see AAW30291). A phage genomic library of strain 12 was screened for clones expressing high molecular strongly reactive choices were subcloned into 77 expression plasmid; all expressed either 125 kDa HWM1 or 120 kDa HWW2 (see Pannid; all expressed either 125 kDa HWM1 or 120 kDa HWW2 (see AAW30294). The expressed proteins are truncated, starting at cresidue 442 of both full-length HWM1 and HWW2 gene products.

Correct processing requires the products of additional downstream genes (see AAY30995 and AAY30995). Nucleotide sequences constructions of see AAY30995 and AAY30995 and AAY30995 and AAY30995 and AAY30997. On the Control of the HWM proteins of non-typeable H.

Influenzae strain 5 (see AAW30291-92) have also been identified.

The HWW proteins, conjugates and peptides can be used as a munogens for preparation of antibodies and as antibodies and as antibodies and be used as to prepare recombinant proteins and as probes for detection of related genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High molecular weight proteins of non-typeable Haemophilus influenzae - useful for vaccine production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This nucleic acid comprises the hmwl gene of non-typeable
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1361 CAGGTGCAGTTATCGACCTTTCAGGTAAAGAAGGGGGAGAAACTTACCTTGGCGGTGACG 1420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1121 AAAATGAAGCGGTCAATCTGGGCGATATTTTGCCAAAGGCGGTAACATTAATGTCCGTG 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1181 CTGCCACTATTCGAAACCAAGGTAAACTTTCTGCTGATTCTGTAAGCAAAGATAAAAGCG 1240
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                         461 TTACIAICITIAGGIGTAACCACTIAGCGITAAAGCCACTITCCGCIAIGTIACTAICIT 520
                                                                                                     520 TAGGTGTAACATCTATTCCACAATCTGTTTTAGCAAGCGGCTTACAAGGAATGGATGTAG 579
                                                                                                                                                                                                         641 ACGCTATCATTAATTGGAAACAATTTAACATCGACCAAAATGAAATGGTGCAGTTTTTAC 700
                                                                                                                                                                                                                                                                  701 AAGAAAACAACAACTCCGCCGTATTCAACCGTGTTACATCTAACCAAATCTCCCAATTAA 760
400 TTGCTGTGTCTGAATTGGCACGGGGTTGTGACCATTCCACAGAAAAAGGCAGCGAAAAAC 459
                                            460 CTGCTCGCATGAAAGTGCGTCACTTAGCGTTAAAGCCACTTTCCGCTATGTTACTATCTT
                                                                                      521 TAGGTGTAACATCTATTCCACAATCTGTTTTAGCAAGCGGCTTACAAGGAATGGATGTAG
                                                                                                                                                581 TACACGGCACAGCCACTATGCAAGTAGATGGTAATAAAAACCATTATCCGCAACAGTGTTG
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2593 GIGTIGATITICACACTICICGCCICAICCICIAACGICCAAACCCCCGGIGTAGITAIAA 2652 ATTCTAAATACTITAATGTTTCAACAGGGTCAAGTTTAAGATTTAAAACTTCAGGCTCAA 2712 2594 GCTCTGTTT-----TTTTTGATATATATGCCAACCATTCTGGCAGAGGGGCTGAGTTAA 2647 2648 AAAIGAGIGAAATTAATATCICTAACGGCGCTAATTITACCITAAATTCCCATGIICGCG 2707 2767 ACATAACACTTTTGCAAGTTGAAGGCACCGATGGAATGATTGGTAAAGGCATTGTAGCCA 2826 2828 CCTACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCAAGCAGCA 2887 3001 GCAACCITACCGCTGGAGGCAATATTGTCAATATAGCCGGAAATCTTACCGTTGAAAGTA 3060 3061 ACGCTAATTTCAAAGCTATCACAAATTTCACTTTTAATGTAGGCGGCTTGTTTGACAACA 3120 3360 ATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTTACCAATG 3187 3188 ATGGTGATTTAAACATTACCACTCACGCTAAACGCAACCAAAGAAGCATCATCGGCGGAG 3247 3181 CCAAGAATTTAAGCATCACCAACTCCAGCTCCACTTACCGCACTATTATAAGCGGCA 3240 3307 3427 3487 3540 3607 3597 3608 AAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTGAAAACAT 3667 3668 CTAGCAGCAATGGCGGACGTGAAAGCAATAGCGACAACGATACCGGCTTAACTATTACTG 3727 2708 GCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCAAATTTCA 2713 CAAAAACTGGCTTCTCAATAGAGAAGATTTAACTTTAAATGCCACC-----GGAGGCA 2888 GCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCCAATAACG CCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTCGTTAATG TTGACAACCATCAAAA----ACCTTTAACTATTAAAAAAGATGTCATTAATAGCG GCGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTTTACCAATA GGAGTTTAAGTTTAACTGGCGAAAATGCAGATATTAAAGGCAATCTCACTATTTCAGAAA 3121 AAGGCAATTCAAATATTTCCATTGCCAAAGGAGGGCTCGCTTTAAAGACATTGATATT ATATCACCAAACAGTAACAATCAAAAAGGGTATTGATGGAGGGGACTCTAGTTGAGTG CGACAAGTAATGCCAACCTAACTATTAAAACCAAAGAATTGAAATTGACAGAAGACCTAA CGACAAACAATGCCAATCTAAACCATTAAAACCAAAGAATTGAAATTAACGCAAGACCTAA GTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTAACTATTG 3548 GCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTTAACAATGTTA 3541 GTAACACCAATAGTGCTGA---TGGTACTAATGCCAAAAAAGTAACCTTTAACCAGGTTA **AAATTGGCGGCAATATCTCGCAAAAAGAAGGCAACCTCACGATTTCTTCCGATAAAATTA** 2653 2768 2948 2947 3008 3128 3308 3068 3368 3488 3428 3421 g δ g δ qq ò qq q δ 셤 qq qq ò ò ò ò pp δ q à qq g ŏ δ Pb Op qq ò δ οχ g ŏ δy g ò

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HMW protein; hmw gene; hmwAl; hmwA2, high molecular weight; mon-typeable Haemophilus influenzae; NTH1, non-eroapsulated; recombinant production; Escherichia coll; antibacterial; vaccine; human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid molecule for producing recombinant high molecular weight proteins of Haemophilus which are used as a vaccine to provide protection against Haemophilus induced diseases in humans -
                                                                                                                                                                                                                                                                             5038 AAGTTCAGTACGGGCTTTACCCATCTTGTAAAAAATTACGGAGAAATAAAATAAGTATT 5097
                          4679 CAACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTA 4738
                                                                                                4739 ATGGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACA 4798
                                                                                                                                                                      4918 ATGCCGCGACGCTGTGCGTTAATATCGCTGATAACGGCCGGTAGCGGTCAGTAATTGACA 4977
                                                                                                                                                                                                    4799 AGGTAGATITCATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTACTGTGTGGGTTA 4858
                                                                                                                                                                                                               4859 AAGTTCAGTACGGGCTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAATTT 4918
4738 TTGAGAAGGTAAAAGATTTATCTGATGAAGAAAGAGAAGCGTTAGCTAAACTTGGAGTAA 4797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "Haemophilus influenzae strain 12 HWWlA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae strain 12 hmwlA gene, SEQ ID NO:66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 16; Fig 28A-Q; 307pp; English.
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351..4961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae strain 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Loosmore SM, Yang Y, Klein MH;
                                                                                                                                                                                                                                                                                                                                                                                                                       AAA52195 standard; DNA; 5116 BP
                                                                                                                                                                                                                                                                                                                                  5098 TTAACAGGTTATTATTATG 5116
                                                                                                                                                                                                                                                                                                                      4919 TTAACAGGTTATTATG 4937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection; diagnosis; ds.
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08-DEC-1998;
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influenzae high molecular weight (HWW) proteins in Escherichia coli. The INTELLINI Intelacts to use tecombinant expression congrises a promoter functional in E. coli (e.g., the T7 promoter) operably linked to a modified humwabc operon from a non-typeable (non-encapsulated) H. clusters termed humwabc operon from a non-typeable (non-encapsulated) H. clusters termed humwabc and humwabc coperon comprises humwabc clusters termed humwabc and humwabc coperon comprises humwabc characters termed humwabc and humwabc coperon comprises humwabc characters termed humwabc accede the structural HWMA proteins cresponsible for post-translational processing and secretion of the HWMA proteins and a gene modified such that it encodes only the proteins. The modified humwabc operon used in the expression construct of mature HWMA proteins (ARB01834-901849) from the non-typeable H. influenzae contrains and secretion of recombinant H. influenzae HWM proteins (ArB01849) from the non-typeable H. influenzae coll-mediated immune response to provide protection against diseases in predensing and tracheobronchitis). The HWM proteins are used for the production of recombinant H. influenzae (coll-mediated immune response to provide protection against diseases in premonia and tracheobronchitis). The HWM proteins are also useful as antigens in immunoassays for detecting antibodies against Haemophilus, HWM proteins and house and the incolates and clone hum and the incolates and clone hum and the model and the incolates and clone hum and the humbanch and the incolates and clone humbanch and the production against Haemophilus, the HWM proteins and coloring the form the model and the production and proved and humbanch and the production against Haemophilus, the HWM proteins and coloring the form the model and the production and proved and proved the model and the production and proved and proved the model and the production and proved the production HMW proteins can be used to isolate and clone hmw genes from other non-typeable strains of Haemophilus via hybridisation reactions. The present sequence represents an hmwA gene from a non-typeable strain of H. invention relates to the recombinant production of Haemophilus 

Sequence 5116 BP; 1766 A; 1008 C; 1037 G; 1305 T; 0 other;

54.3%; Score 2680.2; DB 21; Length 5116; 73.5%; Pred. No. 0; tive 0; Mismatches 1093; Indels 265; Gaps 41 ATGACAAACAACAATTACAACACCTTTTTGCAGTCTATATGCAAATATTTTAAAAAAT 100 161 TITCAICITICAICITICAICITICAICITICAICITICAICITICAICITICAICITICAICITIC 220 101 AGTATAAATCCGCCATATAAAATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATC 160 281 GAATGAAGAGGAGCTGAACGAAACGCAAATGATAAAGTAATTTAATTGTTCAACTAACCT 340 341 TAGGAGAAAATATGAACAAGATATATCGTCTCAAATTCAGCAAACGCCTGAATGCTTTGG 400 401 TTGCTGTGTCTGAATTGGCACGGGGTTGTGACCATTCCACAGAAAAGGCTTCCGCTATG 460 461 TTACTATCTTTAGGTGTAACCACTTAGCGTTAAAGCCACTTTCCGCTATGTTACTATCTT 520 400 TIGCIGIGICIGAATIGGCACGGGCTIGIGACCATICCACAGAAAAAGGCAGCGAAAAAC 459 521 IAGGIGIAACAICIATICCACAATCIGITITAGCAAGCGGCITACAAGGAATGGAIGIAG 580 581 TACACGCCACACCACTATGCAAGTAGATGGTAATAAAACCATTATCCGCAACAGTGTTG 640 460 crecicecardaaagrecercacrrageerraaagecacrrrececrarerracrarerr Matches 3761; Conservative Similarity Query Match В qq à ò 염 ð g ò qq ò g ò g à à

941 TTGTGAATCACGGTTTAATTACTGTCGGTAAAGACGGCAGTGTAAATCTTATTGGTGGCA 1000 1001 AAGTGAAAAACGAGGGTGTGATTAGCGTAAATGGTGGCAGCATTTCTTTACTCGCAGGGC 1060 1121 AAAATGAAGCGGTCAATCTGGGCGATATTTTGCCAAAGGCGGTAACATTAATGTCCGTG 1180 1181 CTGCCACTATTGGAAACCAAGGTAAACTTTCTGCTGATTCTGTAAGGAAAGATAAAAGGG 1240 1180 CTGCCACTATTCGAAACCAAGGTAAACTTTCTGCTGATTCTGTAAGGAAAGATAAAAGCG 1239 1241 GCAATATTGTTCTTTCCGCCAAAGAGGGTGAAGCGGAAATTGGCGGTGTAATTTCCGCTC 1300 641 ACGCTATCATTAATTGGAAACAATTTAACATCGACCAAAATGAAATGGTGCAGTTTTTAC 700 1301 AAAATCAGCAAGCTAAAAGGCGGCAAGCTGATGATTACAGGCGATAAAAGTCACATTAAAAA 1360 1300 AAAATCAGCAAGCTAAAGGGGGCAAGCTGATGATTACAGGCGATAAAGTCACATTAAAAA 1359 1361 CAGGIGCAGITATCGACCITICAGGIAAAGGAGGGGGGGAGAACITACCIIGGGGGGIGACG 1420 1421 AGCGCGGCGAAGGTAAAAACGGCATTCAATTAGCAAAGAAAACCTCTTTAGAAAAAGGCT 1480 1481 CAACCATCAATGTATCAGGCAAAGAAAAAGGCGGACGCGCTATTGTGTGGGGGCGATATTG 1540 701 AAGAAAACAACTCCGCCGTATTCAACCGTGTTACATCTAACCAAATCTCCCAATTAA 760 761 AAGGGATTTIAGATTCTAACGGACAAGTCTTTTAATCAACCCAAATGGTATCACAATAG 820 821 GTAAAGACGCAATTATTAACACTAATGGCTTTACGGCTTCTACGCTAGACATTTCTAACG 880 1420 AGGGGGGGAAGGTAAAAAGGGCATTCAATTAGCAAAGAAAACCTCTTTAGAAAAAGGCT 1479 1541 CGTTAATTGACGGCAATATTAACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTT 1600 1601 TTGTGGAGACATCGGGGCATTATTTATCCATTGACAACGAATGCAATTGTTAAAACAAAG 1660 1661 AGTGGTTGCTAGACCCTGATGATGTAACAATTGAAGCCGAAGACCCCCTTCGCAATAATA 1720 1660 AGTGGTTGTTAGACCCGGATAATGTATCTATTAATGCAGAAACAGCAGGACGCAGCAATA 1719 g ŏ q ò q ò 요 δ g ŏ g ò qq ò g δ g ò q qq ŏ δ g à q δλ Q õ g ò Ω pp ò ò g

1779 1840 1836 1900	1960 1953 2008 2013	2068 2073 2128 2118	2188 2175 2239 2235	2296 2295 2356 2356	2413 2415 2473 2472	533	65	2707	2767 2766 2766	1797
			AGGGCACTGTAACCATTACAGGAGAGAAAGATTTCAGGGCTAACAACGTATCTTTAA	ACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACAATTAACCAAACTACGA	ATCTAGAGACAGGCGCAAATTTTACCTTTATTAAATTACATTTCAAGCAATAGCAAAGC	TGTCATTCAATCTCAAAGAAGGAGCGAAAGTTAATTTCAAATTAAAACCAAACTTAAATGTTGAATTTGAATTTGAATTAAAACCAATAGGGTTTAAATGTTGACATTTAACCAATATGTAATTTAGCAATATGTAATTTAGCAATATTAAATAGCAATTAACGAATTTAAATAGAAACATTTAGGGAATTCGGAATTAAATGAAAACATTTAAATAGAAAAAAAA			3 GCGATGACGCTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCAAATTTCA 3 CAAAAACTGGCTTCTCAATAGAGAAGATTTAATTTTAATTGAAATGCCACCGGAGGGC 3 GCCTTCAGAAGAAGATTTAACTTTAAATGCCACCGGAGGGC 3 GCCTTCAGAAGAAGAAGATTTAACTTAAATGCCAAAGAAGAATTAAAATAAAGAAAG	
1720 1781 1780 1841	0 6 9 6	0 0 0	2129 2119 2189 2176	2240 2236 2297 2296	2357 2356 2414 2416	2474 2473 2534 2533	2594	2648	2708 2713 2768	00/1
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3181 CCAAGAATTTAAGCATCACCACCAACTCCAGCTCCACCTACCGCACTATTATAAGCGGCA 3240 3598 AAGATTCAAAAATCTCTGCTGACGGTCACAAGGTGACACTACACACAGCAAAGTGGAAACAT 3657 3788 C---GGAAAAGGTTACCACCACCAGCAGGCTCGACCATTAACGCAACAATGGCAA---- 3839 3668 CTAGCAGCAATGGCGGACGTGAAAGCAATAGCGACAACGATACCGGCTTAACTATTACTG 3727 3728 CAAAAAATGTAGAAGTAAACAAAGATATTACTTCTCTCAAAACAGTAAATATCACGGGT 3787 3838 AGATAACCGCTCAAACAGGTAGTATCCTAGGTGGAATTGAGTCCAGCTCTGGCTCTGTAA 3897 2827 AAAAAAACATAACCTTTGAAGGAGGTAACATCACCTTTGGCTCCAGGAAAGCCGTAACAG 2886 3001 GCAACCTTACCGCTGGAGGCAATATTGTCAATATAGCCGGAAATCTTACCGTTGAAAGTA 3060 3121 AAGGCAATTCAAATATTTCCATTGCCAAAGGAGGGGCTCGCTTTAAAGACATTGATATT 3180 3188 ATGGTGATTTAAACATTACCACTCACGCTAAACGCAACCAAAGAAGCATCATCGGCGGAG 3247 3248 ATATAATCAACAAAAAGGAAGCTTAAATATTACAGACAGTAATAATGATGTGCTGAAATCC 3307 3308 AAATTGGCGCCAATATCTCGCAAAAGAAGGCAACCTCACGATTTCTTCCGATAAATTA 3367 3368 ATATCACCAAACAGATAACAATCAAAAAGGGTATTGATGGAGAGGACTCTAGTTCAGATG 3427 3428 CGACAAGTAATGCCAACCTAACTATTAAAACCAAAGAATTGAAATTGAAATTGAAAGACCTAA 3487 3488 GTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTAACTATTG 3547 3548 GCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCCAAAACAGTAACTTTTAACAATGTTA 3607 3608 AAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTGAAAACAT 3667 2767 ACATAACACTTTTGCAAGTTGAAGGCACCGATGGAATGATTGGTAAAGGCATTGTAGCCA 2826 2828 CCTACAACATATCCATTCTGGGGGGTAATGTCACCCTTGGTGGACAAAACTCAAGCAGCA 2887 2888 GCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCCAATAAGG 2947 2948 CCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTCGTTAATG 3007 2947 TTGACAACCATCAAAA-----ACCTTTAACTATTAAAAAAGGTGTCATCATTAATAGGG 3000 3008 GGAGTTTAAGTTTAACTGGGGAAAATGCAGATATTAAAGGCAATCTCACAATTTCAGAAA 3067 3068 GCGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTTTACCAATA 3127 3128 ATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTTÄCCAATG 3187 Оp qq Dp q qq Db QQ g g δ g δ рp Qγ g g Ωÿ Dp δλ Dp οy ρp ò qq δ ŏ οy ö δ ò οy δy ò

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4799 AGGTAGATITCAICCIGCAAIGAAGICAIIITAAIIIICGIAIIAITIACIGIGGIIA 4858

3839	957	839	017	898 077	958 137	018 197	078 257	138 317	198 377	258 437	318 497	378 557	438 617	498 677	558 737	618 797	678 857	738 917	798
3840	3898 CACITACIGCAACCGAGGGCGCICITGCTGTAAGCAATAITICGGGCAACACCGTTACIG 3	3840 3	3958 ITACTGCAAATAGCGGTGCATTAACCACTTTGGCAGGCTCTACAATTAAAGGAACCGAGA 4	3840 -AGCAAGTATTACAACCAAAACAGGTGATATCAGGGGTACGATTTCCGGTAACACGGTAA 3   1   1   1   1   1   1   1   1   1	3899 GTGTTAGCGCGACTGGTGATTTAACCACTAAATCCGGCTCAAAAATTGAAGCGAAAATGG 3 	3959 GTGAGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGG 4 	4019 TAAATGTTACGGCAAACGCTGGCGATTAACAGTTGGGGAATGGCGCAGAAATTAATGCGA 4 	4079 CAGAAGGAGCTGCAACCTTAACCGCAACAGGAATACCTTGACTACTGAAGCCGGTTCTA 4	4139 GCATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATGCAGGAA 4 	4199 GCATTANTGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGCT 4	4259 CGGATATTAAAGCAACCAGCGCACCTTGGTTATTAACGCAAAAGATGCTAAGCTAAATG 4 	4319 GTGATGCATCAGGTGATACAGAAGTGAATGCAGCAACGGAAGCGGCTCTGGTAGTG 4 	4379 TGACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGT 4 	4439 TAAATATCATTTCGAAAGATGGTAGAAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGG 4 	4499 TGAAATATTCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCC 4 	4559 TTGAAAAGTAAAAGATTTATCTGATGAAGAAAGAGAAACATTAGCTAAACTTGGTGTAA 4 	4619 GTGCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTTA 4 	4679 CAACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTA 4 	4739 ATGGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACA 4
Qy	QQ	Qy	đ	oy Dp	oy oy	Qy Db	Qy Db	Qy Db	Qy Dp	Qy Db	0y Dp	QZ Dp	oy Dp	<i>∂</i> 8	oy Ob	Oy Db	Oy Dp	67 07	oy Op

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4859 AAGTICAGTACGGGCTTTACCCATCTTGTAAAAATTACGGAGAAATACAATAAAGTATTT 4918
                                                   5038 AAGTICAGTACGGGCTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTT 5097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The isolation and purification of the high molecular weight protein enables the identification of the major protective epitopes of the protein by conventional epitope mapping. These epitopes can then be synthesised using standard techniques and incorporated into fully synthetic or recombinant vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "One of a gene cluster for high molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /notes "One of a gene cluster for high molecular weight protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Possible error in sequence. Alternative sequence for this region is CTTAAATGTT TCCGAGAGTG GCGAGTTTAAA (See AAR41725)"
                                                                                                                                                                                                                                                                                      HMW; high molecular weight protein; virus; vaccine; influenza; epitope; immunity; haemophilus influenzae; gene cluster; ss.
                                                                                                                                                                                                                                                                                                                                                                                              'product - High molecular weight protein 1.
                                                                                                                                                                                                                                                           Gene cluster for high molecular weight protein 1 (HMW1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High molecular weight surface proteins - of non-typeable haemophilus which exhibit immunogenic properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAR41725, AAR41726, AAR41727.
                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Figure 6; 100pp; English.
                                                                                                                                                                                 AAQ49508 standard; DNA; 9220 BP.
                                                                                                     5098 TTAACAGGTTATTATTATG 5116
                                                                                        4919 TTAACAGGTTATTATG 4937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93WO-US02166.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2351..2380
                                                                                                                                                                                                                                   26-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7062..9011
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                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barenkamp SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-SEP-1993.
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                                                                                                                                                       RESULT 12
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1121 AAAATGAAGCGGTCAATCTGGGCGATATTTTGCCAAAGGCGGTAACATTAATGTCCGTG 1180 1361 CAGGIGCAGTTATCGACCTTTCAGGTAAAGAAGGGGGAGAAACTTACCTTGGCGGTGACG 1420 1601 TTGTGGAGACATCGGGGCATTATTTATCCATTGACAGCAATGCAATTGTTAAAACAAAAG 1660 1100 TTGTGGAGACGTCGGGGCATGATTATTCATCAAAGACAATGCAATTGTTGACGCCAAAG 1659 1000 AAGTGAAAAACGAGGGTGTGATTAGCGTAAATGGTGGCAGCATTTTTTACTCGCAGGGC 1059 1181 CTGCCACTATTCGAAACCAAGGTAAACTTTCTGCTGATTCTGTAAGCAAAGATAAAAGCG 1240 1241 GCAATATTGTTTTTCCGCCAAAGAGGGTGAAGCGGAAATTGGCGGTGTAATTTCCGCTC 1300 1301 AAAATCAGCAAGCTAAAAGGCGGCAAGCTGATGATTACAGGCGATAAAGTCACATTAAAAA 1360 1360 CAGGTGCAGTTATCGACCTTTCAGGTAAAGAAGGGGGAGAAACTTACCTTGGCGGTGACG 1419 1421 AGCGCGCGAAGGTAAAAACGGCATTCAATTAGCAAAGAAAACCTCTTTAGAAAAAGGCT 1480 1481 CAACCATCAATGTATCAGGCAAAGAAAAAGGCGGACGCGCTATTGTGTGGGGGGGATATTG 1540 1541 CGTTAATTGACGGCAATATTAACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTT 1600 1661 AGTGGTTGCTAGACCCTGATGATGTAACAATTGAAGCCGAAGACCCCCTTCGCAATAATA 1720 1720 CTTCAGAAGACGATGAATACACGGGATCCGGGAATAGTGCCAGCACCCCAAAACGAAACA 1779 1781 GCGAACTCAAAACAACGCTAACCAATACAACTATTCAAATTATCTGAAAAACGCCTGGA 1840 1837 TIGITAACATCACTGCTAATCAACGCATCTATGTCAATAGCTCCATTAATTT---ATCCA 1893 1901 ACTCCCACTTAATTCTCCATAGTAAAGGTCAGCGTGGCGGAGGCGTTCAGATTGATGGAG 1960 1961 ATATTAC -----TTCTAAAGGCGGAAATTTAACCATTTATTCTGGCGGATGGG 2008 2009 TIGATGTICATAAAAATATTACGCTIGATCAGGGTITITTAAATATTACCGCCGCTICCG 2068 2014 TTGATGTTCATAAAAATATCTCACTCGGGGGGCGAAGGTAACATAAACATTACAGCTAAAC 2073 2069 TAGCTTTTGAAGGTGGAAATAACAAAGCACGCGACGCGGCAAATGCTAAAATTGTCGCCC 2128

AGGGGAGTGGGAGTGGATTGACCACTAAÀACAACAÀTTAAATACCTATAGA AGAACACTGGATTGACATTAAATATTGGGGAAATTAAACATCAACAATTAACACTAAACACAATTAAATATTGGGGAAATTTAACATGAAATTGGGAAATTTAACATGAAATTTAAAGGGAAATTTAACAGGAAATTTAACAGGAAATTTAAAGGCAAATTTAAAAGGCAAATTTAAAGGCAAATTTAAAGGCAAATTAAAAGGCAAATTTAAAGGCAAATTTAAAGGCAAATTTAAAAAAGCAAAATTAAAAAAGGCAAATTTAAAGGCAAATTTAAAAAAAGCAAAAATTAAAGGCAAATTTAAAGGCAAATTTAAAAAAAA	0 0 0		2188 2175 2239
235 241 241 241 241 241 241 241 253 264 265 265 265 266 267 267 268 268 268 268 268 268 268 268	ACGGC ACAAT ATAA	ACGGCACTGGCAGCTGCAATTCACCACTAAAAGAACCAATAAATA	2 2 3
241 241 247 247 253 253 253 253 253 253 253 253 253 253	GAAA     	GAACACCTCGTATTGGCAAACCAGCCATGATTCGCACTGGAACGTCAGTGCTCTTA	35
2477 2533 2593 2593 2647 2707 2707 2707 2707 2707 2707 2707 27	ATCT TGGA	AGAGACAGGCGCAAATTTTACCTTTATTAAATACATTTCAAGCAATAGCAAAGG	2413
	GCTT 	AACAACACTATAGAAGCTCTGCAGGGGTGAATTTTAACGGCGTAAATGGCAACA 	7 7
	TGT   TTA	CATTCAATCTCAAAGAAGGAGCGAAAGTTAATTTTCAAATTAAAACCAAACGAGAACA 	53
	TGAI   AGTI	ACACAAGCAAACCITTACCAATTCGGTTTTTAGCCAATATCACAGCCACTGGTGGGG 	59 59
	GCT   GTG	CTGTTTTTTTTGATATATGCCAACCATTCTGGCAGAGGGCTGAGTTAA	2647
	AAA   ATT	TGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCCCATGTTCGCG 	2707
	GCG	ATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCAATTTCA 	2767 2766
	GCC.	TCAGACAGAAGAAGATTTTTATGACGGGTACGCACGCAATGCCATCAATTCAA 	2827 2826
	CCT	ACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCAAGCAGCA 	2887 2886
	GCA       	TTACGGGGAATATTACTATCGAGAAGCAGCAAATGTTACGCTAGAAGCCAATAACG 	2947
	CCC	CTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGGCAGCTTGCTCGTTAATG	3007
	GGA(		3067
318	GCG ACG		3127
	ATG - AAG	SCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTTACCAATG 	3187 3180

ολ	3188	GATTTAAACATTACCACTCACGCTAAACGCAACCAAAGAAGCATCATCGGCGG	324
QQ	3181	TTTAAGCATCACCACCAACTCCAGCTCCACTTACCGCACTATTATAAGCG	324
Qy Dp	3248	GAAATCC 	330.
δy	308	AAAATTA	n m
qq	3301	AAAATCA	336(
δy	3368	TCAGATG	
qq	3361	TCAGACG	
ογ	428	GACCTAA	348
QQ	3421	SACCTAA	4
δ	3488	ACTATTG	2
QQ	81	ACTATIG	ß
ΟŊ	3548	AATGTTA	3607
Op	3541	AGGTTA	2
Qy Dp	3598	AACAT	
οy	668	ATTACTG	_
qq	658	II II	3717
δλ	28	ACCGCGT	7
QQ	18	rcrecea	3777
οy	œ	A.A	æ
ΩD	3778	AACGTGG	œ
δy	3840		
QΩ	3838	CTGTAA	
οy	3840		3835
qq	3898	STTACTG	3957
Qy	3840		8
qq	3958	ACCGAGA	4017
Qy	3840	AGTATTACAACCAAAACAGGTGATATCAGCGGTACGATTTCCGGTAACACGGTAA	8
qq	4018	CACTTCAAGTCAATCAGGCGATATCGGCGGTACGATTTCTGGTGGTGGCACAGTAG	0
δy	3899	AGCGCGGCTGGTGTTTAACCACTAAATCCGGCTCAAAAATTGAAGCGAAATCGG	3958
qq	4078	TTAAAGCAACCGAAAGTTTAACCACTCAATCCAATTCAAAATTAAAGCAACAACAG	-
οy	3959	GCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACG	4018
QQ	4138	CGAGGCTAACGTAACAAGTGCAACAGGTACAATTGGTGGTGGTTTCCGGTAATACGG	4197
δ d	4019	AACAGTTGGGAATGGCGCAGAAATTAATGCGA	4078
6	· ~	AGAAGGAGCTGCAACCTTAACCGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCT	4138

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4258 CAGAAGGAGCTGCAACCTTAACTACATCATCGGGCAAATTAACTACCGAAGCTAGTTCAC 4317
                                             4139 GCATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAA 4198
                                                               4199 GCATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGCT 4258
                                                                                                                           4259 CGGATATTAAAGCAACCAGCGCACCTTGGTTATTAACGCAAAAGATGCTAAATG 4318
                                                                                                                                                                                        4438 CAAACATTAATGCAACCAGCGGTACCTTGGTTATTAACGCAAAAGACGCTGAGCTAAATG 4497
                                                                                                                                                                                                                                4319 GTGATGCATCAGGTGATAGTACAGAAGTGAATGCAGTCAACGCAAGCGGCTCTGGTAGTG 4378
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                                                                                                                                                                                                                                                                                                              4439 TAAATATCATTTCGAAAGATGGTAGAAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGG 4498
                                                                                                                                                                                                                                                                                                                                                                                 4618 TAAATATCATTTCAAAAAACGGTATAAAACCCCTACTATAAAAGCGGTTAAAATTGATG 4677
                                                                                                                                                                                                                                                                                                                                                                                                                       4499 TGAAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCC 4558
                                                                                                                                                                                                                                                                                                                                                                                                                                           4559 TTGAAAAAGTAAAAGATTTATCTGATGAAGAAAGAGAAACATTAGCTAAACTTGGTGTAA 4618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4738 TIGAGAAGGTAAAAGATTTATCTGATGAAGAAGAGAAGCGTTAGCTAAACTTGGCGTAA 4797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4739 ATGGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACA 4798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4799 AGGTAGATTICATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTACTGTGTGGGTTA 4858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4978 AGGIAGALTICATCCIGCAATGAAGICATTITITITITITITATTITACIGIGGGITA 5037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-typeable Haemophilus; high molecular weight surface protein; HMW1; hmw1 gene; immunogen; vaccine; otitis media; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5098 TTAACAGGTTATTATTATG 5116
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This nucleic acid comprises a gene cluster for the hmw1 gene (see also ART90994) that encodes high molecular weight surface protein IMM1 (see AAW30293) of non-typeable Haemophilus influenzes strain 12. In addition to the hmw1 gene there are 2 additional downstream open reading frames that are required for the correct processing and secretion of the hmw1 gene product. The ORF-b derived amino acid sequence demonstrates similarity with the derived amino acid sequences of 2 genes which encode proteins required for secretion and activation of haemolysins of P. mirabilis and S. marcescens. HWM proteins (see AAW30291-44) can be used in vaccines, as immunogens for preparation of antibodies and as antigens for detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 ATGACAAACAACAATTACAACACCTTTTTTGCAGTCTATATGCAAATATTTTAAAAAAT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 AGTATAAATCCGCCATATAAAATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATC 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 TITCATCTITCATCTITCATCTITCATCTITCATCTITCATCTITCATCTITCATCTITC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281 GAATGAAGAGGAGCTGAACGAACGCAAATGATAAAGTAATTTAATTGTTCAACTAACCT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52.0%; Score 2565.4; DB 18; Length 9171; rilarity 72.4%; Pred. No. 0; Conservative 0; Mismatches 1096; Indels 315; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High molecular weight proteins of non-typeable Haemophilus influenzae - useful for vaccine production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9171 BP; 3085 A; 1855 C; 1794 G; 2437 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 78-82; 183pp; English.
                                                      /*tag= a
5104..6*hmw1 gene"
5104..6748
/*tag= b
7062..9011
/*tag= "ORF-b"
/*tag= "ORF-c"
                           Location/Qualifiers
351..4958
Haemophilus influenzae strain 12.
                                                                                                                                                                                                                                                                96US-0617697.
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                                                                                                                                                                                                                                                                                           (BARE/) BARENKAMP S J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for preparation these antibodies.
                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW30293
                                                                                                                                                                                                                                                                                                                      Barenkamp SJ;
                                                                                                                                                                               WO9736914-A1.
                                                                                                                                                                                                                                    01-APR-1997;
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                                                                                                                                                                                                         09-OCT-1997.
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340	TAGGAGAAAATATGAACAAGATATATCGTCTCAAATTCAGCAAACGCCTGAATGCTTTGG 399	
401	TTGCTGTGTCTGATTGGCACGGGGTTGTGACCATTCCACAGAAAAGGCTTCCGCTATG 460 	
461	THACTATCTTTAGGTGTAACCACTTAGGGTAAAGCCACTTTCCGGTATGTTACTT 520   1	
521 520	TAGGTGTAACATCTATTCCACAATCTGTTTTAGCAAGGGGCTTACAAGGAATGGATGTAG 580 	
581 580	TACACGCCACAGCCACTATGCAAGTAGATGGTAATAAAACCATTATCCGCAACAGTGTTG 640 	
641	ACGCTATCATTAATTGGAACAATTTAACATCGACCAAAATGAAATGGTGCAGTTTTTAC 700 	
701	AAGAAAACAACAACTCCGCCGTATTCAACGGTGTTACATCTAACCAAATCTCCCAATTAA 760 	
761 760	AAGGGATTTTAGATTCTAAGGGACAAGTCTTTTTAATCAACCCAAATGGTATCACAATAG 820 	
821 820	GTAAAGACGCAATTATTAACACTAATGGCTTTACGGCTTCTACGCTAGACATTTCTAACG 880 	
881	AAAACATCAAGGGGGTAATTTCACCTTCGAGCAAACCAAGATAAAGGGCTCGCTGAAA 940 	
941	TTGTGAATCACGGTTTAATTACTGTCGGTAAAGACGCAGTGTAAATCTTATTGGTGGCA 1000 	
 1001	AAGTGAAAAACSAGGGTGTGATTAGCGTAAATGGTGCAGCAGCATTCTTTACTCGCAGGC 1060 	
 1061 1060	AAAAAATCACCATCAGCGATATAATAAACCCAACCATTACTTAC	
 1121	AAAATGAAGGGTCAATCTGGGGGATATTTTTGCCAAAGGGGGTAACATTAATGTCGGT 1180 	
 1181	CTGCCACTATTCGAAACCAAGGTAAACTTTCTGCTGATTCTGTAAGCAAAGATAAAAGG 1240 	
 1241	GCAATATTGTTCTTTCCGCCAAAGAGGGTGAAGCGGAAATTGGCGGTGTAATTTCCGCTC 1300	
 1301 1250	AAARCAGCAAGCTAAAGGGGGCAAGCTGATGATTACAGGCGATAAAGTCACATTAAAAA 1360 	
 1361 1310	CAGGIGCAGTTATCGACCTTTCAGGTAAAGAGGGGAGAAAACTTACCTTGGGGGTGAGG 1420 	
1421	AGCGCGGCGAAGGTAAAAACGCCATTCAATTAGCAAAGÀAAACCTCTTTAGAAAAGGCT 1480 	

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2423 TJAATGTTGAACGAAGGGAAGAGTCAACTTTGACATCAAGGCACCAATAGGGATAAATA 2482
1370 AGCGCGCGAAGGTAAAAACGCATTCAATTAGCAAAGAAAACCTCTTTAGAAAAGGCT 1429
                                                                                                                                    1541 CGTTAATTGACGGCAATATTAACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTT 1600
                                                                                                                                                                                     1490 CGTTAATTGACGCCAATATTAACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTT 1549
                                                                                                                                                                                                                                1601 TTGTGGAGACATCGGGGCATTATTATCCATTGACAGCAATGCAATTGTTAAAACAAAAG 1660
                                                                                                                                                                                                                                                      1661 AGTGGTTGCTAGACCCTGATGATGTAACAATTGAAGCCCGAAGACCCCCTTCGCAATAATA 1720
                                                                                                                                                                                                                                                                                                                                                  1670 CTTCAGAAGACGATGAATACACGGGATCCGGGAATAGTGCCAGCACCCCAAAACGAAACA 1729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1904 ATATTACCACCGGTGATGATACCAGAGGTGCAAACTTAACAATTTACTCAGGCGGCTGGG 1963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2009 ITGAIGTICATAAAAATATTACGCTTGATCAGGGTTTTTTAAATATTACCGCCGCTTCCG 2068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2069 TAGCTTTTGAAGGTGGAAATAACAAAGCACGCGACGCGGCAAATGCTAAAATTGTCGCCC 2128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2129 AGGGCACTGTAACCATTACAGGAGAGAAAAGATTTCAGGGCTAACAACGTATCTTTAA 2188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2069 AAGGGACTATTACC---TCAGGCAATCAAAAAGGTTTAGATTTAATAATGTCTCTATAA 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2189 ACGGAACGGGTAAAGGTCTGAATATCATTTCATCAGGGAATAATTTA------ACCC 2239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2240 ACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACAATTAACCAAACTA---CGA 2296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2297 GAAAGAACACCTCGTATTGGCAAACCAGCCATGATTCGCACTGGAACGTCAGTGCTCTTA 2356
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3788 C---GGAAAAGGTTACCACCACAGCAGGCTCGACCATTAACGCAACAATGGCAA---- 3839 3728 CAAGTGGAGAAATTACCACTAAAACAGGTACCATTAACGCAACCACTGGTAACGTGG 3787 3840 ----- 3839 3840 -AGCAAGTATTACAACCAAAACAGGTGATATCAGCGGTACGATTTCCGGTAACACGGTAA 3898 3968 GTGTAACCACTTCAAGTCAATCAGGCGATATCGGCGGTACGATTTCTGGTGGCACAGTAG 4027 3899 GTGTTAGCGCGACTGGTGATTTAACCACTAAATCCGGCTCAAAATTGAAGGGAAATCGG 3958 4028 AGGTTAAAGCAACGAAAGTTTAACCACTCAATCCAATTCAAAAATTAAAGCAACAACA 4087 4019 TAAATGTTACGGCAAACGCTGGCGATTTAACAGTTGGGAATGGCGCAGAAATTAATGCGA 4078 4079 CAGAAGGAGCTGCAACCTTAACCGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCTA 4138 4199 GCATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGCT 4258 3668 CTAGCAGCAATGGCGGACGTGAAAGCAATAGCGACAACGATACCGGCTTAACTATTACTG 3727 3608 CCGGTAGTAATAACAACACTGAAGATAGCAGTGACAATAATGCCGGCTTAACTATCGATG 3667 3728 CAAAAAATGTAGAAGTAAACAAAGATATTACTTCTCTAAAACAGTAAATATCACCGCGT 3787 3668 CAAAAAATGTAACAGTAAACAACAATATTACTTCTCACAAAGCAGTGAGCATCTCTGCGA 3727 3788 AGATAACCGCTCAAACAGGTAGTATCCTAGGTGGAATTGAGTCCAGCTCTGGCTCTGTAA 3847 3848 CACTTACTGCAACCGAGGCGCTCTTGCTGTAAGCAATATTTCGGGCAACACCGTTACTG 3907 3840 ----- 3839 3908 TTACTGCAAATAGCGGTGCATTAACCACTTTGGCAGGCTCTACAATTAAAGGAACCGAGA 3967 3959 GTGAGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGG 4018 4328 GTATTAATGCCGCCAATGTGACACTAAATACTACAGGCACTTTAACTACCGTGAAGGGTT 4387 4259 CGGATATTAAAGCAACCAGCGCACCTTGGTTATTAACGCAAAAGATGCTAAGCTAAATG 4318 4319 GTGATGCATCAGGTGATACTACAGAAGTGAATGCAGTCAACGCAAGCGGCCTCTGGTAGTG 4378 4379 TGACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGT 4438 4439 TAAATATCATTTCGAAAGATGGTAGAAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGG 4498 4448 GCGCAGCATTGGGTAACCACACAGTGGTAAATGCAACGCAACGCAAATGGCTCCGGCAGCG 4507 4568 TAAATATCATTTCAAAAAACGGTATAAACACCGTACTGTTAAAAGGCGTTAAAATTGATG 4627 4499 TGAAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCC 4558 qq Dp g Qγ q ŏ g δλ qq g οy Db οý q δ g g ŏ qq ò Db qq qq g ò ò οy Q οy ò

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4628 TGAAATACATTCAACCGGGTATAGCAAGCGTAGATGAAGTTGAAGTGAAGCGAAACGCATCC 4687
                                        4559 TTGAAAAAGTAAAAGATTTATCTGATGAAGAAAGAGAAAACATTAGCTAAACTTGGTGTAA 4618
                                                                   4688 TTGAGAAGGTAAAAGATTTATCTGATGAAGAAAGAGAAGCGTTAGCTAAACTTGGCGTAA 4747
                                                                                               4619 GTGCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTTA 4678
                                                                                                               4679 CAACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTA 4738
                                                                                                                                                                   4739 ATGGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACA 4798
                                                                                                                                                                                                                                                                   4799 AGGTAGATITCATCCTGCAATGAAGTCATTTTATITITCGTATTATTTACTGTGTGGGTTA 4858
                                                                                                                                                                                                                                                                                    4859 AAGTICAGTACGGGCTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTT 4918
                                                                                                                                                                                                                                                                                                                                         Non-typeable Haemophilus high mol.wt. surface protein HMW4 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Non-typeable Haemophilus; high molecular weight surface protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High molecular weight proteins of non-typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /transl_except= (pos:1114..1116, aa:Thr)
/transl_except= (pos:1198..1200, aa:Asp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMW4; immunogen; vaccine; otitis media; ss
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1..4803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemophilus influenzae strain 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT90993 standard; DNA; 4803 BP
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2 Novel nucleic acids (AAT90992 and AAT90993) respectively comprise the coding sequences of high molecular weight surface proteins HWW3 (see AAW30291) and HWW4 (see AAW30292) of Haemophilus influenzae strain 5. HWW3 has a mol.wt. of 125 KDa and HWW4 has a mol.wt. of 123 KDa. Both are antiquically related to HWM1 (see AAW30293) and HWW2 (see AAW30294) obtained from non-typeable H. influenzae strain 12 Vectors containing HWW nucleic acids for transformation of a host detection of related genes. HWW proteins, conjugates and peptides can be used in vaccines, as immunogens for preparation of
                                                                                                                                                                                                                                                                                                                                 Query Match 45.5%; Score 2245; DB 10; Length 4803; Best Local Similarity 70.6%; Pred. No. 0; Matches 3411; Conservative 0; Mismatches 990; Indels 432; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  952 GGTTTAATTACTGTCGGTAAAGACGGCAGTGTAAATCTTATTGGTGGCAAAGTGAAAAAC 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1012 GAGGGTGTGATTAGCGTAAATGGTGGCAGCATTTCTTTACTCGCAGGGCAAAAAATCACC 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GAATTGACACGGGGTTGTGACCATTCCACAGAAAAGGCAGTGAAAAACCTGTTCGTACG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 AAAGTACGCCACTTGGCGTTAAAGCCACTTTCCGCTATATTGCTATCTTTGGGCATGGCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 661 GAGGCGTGATTAGCGTAAATGGCGGTAGTATTTCTTTACTTGCAGGGCAAAAATCACC 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          532 TCTATTCCACAATCTGTTTTAGCAAGCGGCTTACAAGGAATGGATGTAGTACACGGCACA 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GCAACCATGCAAGTAGACGGCAATAAAACCACTATCCGTAATAGCGTCAATGCTATCATC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              652 AATTGGAAACAATTTAACATCGACCAAAATGAAATGGTGCAGTTTTTACAAGAAAACAAC 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      712 AACTCCGCCGTATTCAACCGTGTTACATCTAACAAATCTCCCAATTAAAAGGGATTTTA 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 AACTCTGCCGTTTTCAACCGTGTTACATCTGACCAAATCTCCCAATTAAAAGGGATTTTA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 GAATTGGCACGGGGTTGTGACCATTCCACAGAAAAAGGCTTCCGCTATGTTACTATCTTT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 AGGTGTAACCACTTAGCGTTAAAGCCACTTTCCGCTATGTTACTATCTTTAGGTGTAACA 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   592 GCCACTATGCAAGTAGATGGTAATAAAACCATTATCCGCAACAGTGTTGACGCTATCATT 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 772 GATTCTAACGGACAAGTCTTTTTAATCAACCCAAATGGTATCACAATAGGTAAAGACGCA 831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGAACAAGATATATGTCGTCTCAAATTCAGCAAACGCCTGAATGCTTTGGTTGCTTGTGTCT 60
                                                                                                                                                                                                                                        antibodies and as antigens for detection of these antibodies.
                                                                                                                                                                                                                                                                                      Sequence 4803 BP; 1714 A; 928 C; 971 G; 1190 T; 0 other;
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2206 CIGAAIAICATITCAICAGIGAAIAAITIAACCCACAAICTIAGIGCCACAAITAACAIA 2265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2086 AATAACAAAGCACGGAGCGGCAAATGCTAAAATTGTCGCCCAGGGCACTGTAACCATT 2145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1726 GGCGATAAAGCACGTAACGCAACAGATGCTCAAATTACCGCACAAGGGACGATAACCGTC 1785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2029 ACGCTIGAICAGGGITITITAAAIAITACCGC---CGCTICCGIAGCTTIGAAGGIGGA 2085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1555 ACACTICACACTAAA-----CGAGAIGGAGTIAAAATIAACGGIGATATIACCICA 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1972 a---aaggcggaaattfaaccaittattctggcggatgggttgatgttcataaaatatt 2028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1498 ACTGCTAATAATAGAATTTATGTTAATAGCTCCATCAACTT ---ATCTAATGGCAGTTTA 1554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1792 ACAACGCTAACCAATACAACTATTTCAAATTATCTGAAAAACGCCTGGACAATGAATATA 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1438 CCTACATTAACAAACTCAACTCTTGAGCAAATCCTAAGAAGAGGTTCTTATGTTAATATC 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1672 GACCCTGATGAACAATTGAAGCCGAAGACCCCTTCGCAATAATACCGGTATAAAT 1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1318 GACCCAGATGATGTGCCATTGAAACTCTTACATCTGGACGCAATAATACGGGCGAAAAC 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1612 TCGGGGCATTATTTATCCATTGACAGCAATGCAATTGTTAAAACAAAAGAGTGGTTGCTA 1671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1258 TCAGGACATGACTTATCCATTGGTGATGATGATGATGATGATGACGCTAAAGAGTGGTTATTA 1317
                                                                                                                                                                                                                                                                                                                                                                            1552 GGCAATATTAACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGGAGACA 1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1081 GGTAAAAATGGTATTCAATTAGCGAAGAAAACCTCTTTAGAAAAAGGCTCGACAATTAAT 1140
                                                                                                                                                                                                                                                                                                                                                         1492 GTATCAGGCAAAGAAAAAGGCGGACGCGCTATTGTGTGGGGCGATATTGCGTTAATTGAC 1551
                                                                                                                                                                                                                                   1432 GGTAAAAAGGGCATTCAATTAGCAAAGAAAACCTCTTTAGAAAAAGGCTCAACCATCAAT 1491
                                                                                                                                                           1372 ATCGACCITICAGGTAAAGAAGGGGGAGAAACTTACCITGGGGGTGACGAGGGCGGGAA 1431
1312 GCTAAAGGCGGCAAGCTGATGATTACAGGCGATAAAGTCACATTAAAAACAGGTGCAGTT 1371
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3331 AAAGAAGGCAACCTCACGATTTCTTCCGATAAAATTAATATCACCAAACAGATAACAATC 3390 3211 CAGGCTAAACGCAACCAAAGAAGCATCATCGGCGGAGATATAATCAACAAAAAAAGGAAGC 3270 3154 CAAGGAGTGGTAAAACT --- TGGCAATGTTACCAATGATGGTGATTTAAACATTACCACT 3210 2806 CAAGGAGTGGTAAAACTCCAAGGCGATATTATCAATAAAGGTGGTTTAAATATCACTACT 2865 3094 GATACCCTAAATATCACCGGCAATTTTACCAATAATGGCACTGCCGAAATTAATATAACA 3153 2626 AGAACTCTAACTCTTGGCAATATATCTGTTGAGGGGAATTTAAGCCTAACTGGTGCAAAT 2685 3034 GCAGATATTAAAGGCAATCTCACTATTTCAGAAAGCGCCACTTTTAAAGGAAAGACTAGA 3093 111 | 111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 2974 AGAGTIATAAAACTTGGCAGCTTGCTCGTTAATGGGAGTTTAAGTTTAACTGGCGAAAAT 3033 2914 AAAGCAGCAAATGTTACGCTAGAAGCCAATAACGCCCCTAATCAGCAAAACATAAGGGAT 2973 2566 AATAAAGGAAATGTTACATTACAAGGTGACAGCAAGAAGAGAAGAGGGTTGAAAAA 2625 2854 AATGTCACCCTTGGTGGACAAAACTCAAGCAGCAGTACGGGGAATATTACTATCGAG 2913 2386 GACTTAACTATAAATGCAACTGGCTCGAATTTTAGTCTTAAGGAAAGGAAAGATTCTTT 2445 2794 TATGACGGGTACGCACGCAATGCCATCAATTCAACCTACAACATATCCATTCTGGGCGGT 2853 111 | 1 | 1 | 1 | 1 | 1 | 2446 TATAATGAAATCATTAACCATTAACGGGC 2505 2734 GACTTAACCATAAATGCAACCAATTCAAATTTCAGCCTCAGACGAAAGATGATTT 2793 2674 GGCGCTAATTTAACTTAAATTCCCATGTTCGCGGCGATGACGCTTTTAAAATCAACAAA 2733 2560 CGGTTTTTAGCCAATATCACAGCCACTG-----GTGGGGGCTCTGTTTTTTTTATATA 2613 2614 TATGCCAACCATTCTGGCAGAGGGGCTGAGTTAAAATGAGTGAAATTAATATCTCTAAC 2673 2266 cacGCCAATCTTACCTCTAGAGCTGCCGGCATAAACATGGATTCAATTAACATTACGGC 2325 2500 AAAGTTAATTTCAAATTAAAACCAAACGAGAACATGAACACAAGCAAACCTTTACCAATT 2559 2440 GCAGGGGTGAATTTTAACGGCGTAAATGGCAACATGTCATTCAATCTCAAAGAAGGAGGG 2499 2086 GCAGGCGTACATTTAACGGCATCGGAGGCAAAACAAACTTCAACATCGGAGCTAACGCA 2145 2386 ATTAAATACATTTCAAGG-----AATAGCAAAGGCTTAACAACAGTATAGAAGCTCT 2439 2026 ATABAATTGGTTGATAGGGGTCAAATTCCCAAGATTTGAGGTCATCACGTAGAGTTTT 2085 2326 CATGATTCGCACTGGAACGTCAGTGCTCTTAATCTAGAGACAGGCGCAAATTTTACCTTT qq Ω Ob ò òγ g qq Ω qq δ qq Ωy Qγ QQ οy qq Dp ò g δλ Op δŏ δλ Db δy Оp φ g q ò αq ð

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4051 GCAAGCACTGGTGATTTAACTATTGGAAATAGTGCAAAAGTTGAAGCGAAAAATGGAGCT 4110
                              4090 GCAACCTTAACCGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCTAGCATCACTTCA 4149
                                                       4150 ACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAAGCATTAATGCT 4209
                                                                    4210 GCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGCTCGGATATTAAA 4269
                                                                                                       4270 GCAACCAGCGGCACCTTGGTTATTAACGCAAAAGATGCTAAGCTAAATGGTGATGCATCA 4329
                                                                                                                                           4330 GGTGATAGTAGAAGTGAATGCAGTCAACGCAAGCGGCTCTGGTAGTGTGACTGCGGCA 4389
                                                                                                                                                                                                                     4390 ACCICAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGTTAAATATCATT 4449
                                                                                                                                                                                                                                                        4450 TCGAAAGATGGTAGAAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGGTGAAATATATC 4509
                                                                                                                                                                                                                                                                                            4510 CAGCCAGGTGTAGCAAGTGTAGAAGTAATTGAAGCGAAACGCGTCCTTGAAAAGTA 4569
                                                                                                                                                                                                                                                                                                                      4570 AAAGATTTATCTGATGAAGAAAAAAACATTAGCTAAACTTGGTGTAAGTGCTGTACGT 4629
                                                                                                                                                                                                                                                                                                                                  4630 TTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTTACAACCAGACCG 4689
                                                                                                                                                                                                                                                                                                                                                                       Partial sequence encoding high molecular weight protein 4 (HMW4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HMW; high molecular weight protein; virus; vaccine; influenza; epitope; immunity; haemophilus influenzae; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= High molecular weight protein 4.
misc_difference 899.901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
/transl_except= TCT encodes Threonine.
                                                                                                                                                                                                                                                                                                                                                                                                                                    4750 GTATGTACCAATGTTGCTGACGATGGACAGCCG 4782
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ49511 standard; DNA; 4702 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae.
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Barenkamp SJ;

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30-SEP-1993. WO9319090-A.

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1019 AAAACTGGGGGCTTTGTGGAAACATCAGGACATGACTTATCCATTGGTGATGTGATT 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1319 AACTI---ATCTAATGGCAGTTTAACACTTCACACTAAA------CGAGATGGAGTT 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1199 CCTAAAGGTAATAGTATTTCTAAACCTACATTAACAAACTCAACTCTTGAGCAAATCCTA 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1259 AGAAGAGGTTCTTATGTTAATATCACTGCTAATAATAGAATTTATGTTAATAGCTCCATC 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1888 AACATCGGAAGCAACTCCCACTTAATTCTCCATAGTAAAGGTCAGCGTGGCGGAGGCGTT 1947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1367 AAAATTAACGGTGATATTACCTCAAACGAAAATGGTAATTTAACCATTAAAGCAGGCTCT 1426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1487 GATTCTGTAGCTTTTGAGAGAGGGGGGGTAAAGCACGTAACGCAACAGATGCTCAAATT 1546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2122 GTCGCCCAGGGCACTGTAACCATTACAGGAAAAAGATTTCAGGGCTAACAACGTA 2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1528 TGGGGCGATATTGCGTTAATTGACGGCAATATTAACGCTCAAGGTAGTGGTGATATCGCT 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1768 CCTAAAAAAAATAGCGAACTCAAAACAACGCTAACCAATACAACTATTTCAAATTATCTG 1827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1828 AAAAACGCCTGGACAATGAATATAACGGCATCAAGAAAACTTACCGTTAATAGCTCAATC 1887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1948 CAGATTGATGGAGATATTACTTCTA---AAGGCGGAAATTTAACCATTTATTCTGGCGGA 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2005 TGGGTTGATGTTCATAAAAATATTACGCTTGATCAGGGTTTTTTAAATATTACCGC---C 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2062 GCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGCGGCGGCGAAATGCTAAAATT 2121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2182 TCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCATCAGTGAATAATTTAACCCAC 2241
  1108 ATTGCCGCGCCTGAAAATGAAGCGGTCAATCTGGGCGATATTTTTGCCAAAGGCGGTAAC 1167
                                                                                             1168 ATTAATGTCCGTGCTGCCACTATTCGAAACCAAGGTAAACTTTCTGCTGATTCTGTAAGC 1227
                                                                                                                                                                                         1228 AAAGATAAAAGCGGCAATATTGTTCTTTCCGCCAAAGAGGGGTGAAGCGGAAATTGGCGGT 1287
                                                                                                                                                                                                                                                                                 1288 GTAATTTCCGCTCAAAATCAGCAAGCTAAAGGCGGCCAAGGTGATGATTACAGGCGATAAA 1347
                                                                                                                                                                                                                                                                                                                                                                             1348 GTCACATTAAAAACAGGTGCAGTTATCGACCTTTCAGGTAAAGAAGGGGGGAAAACTTAC 1407
                                                                                                                                                                                                                                                                                                                                                                                                     1408 CTTGGCGGTGACGAGCGCGGCGAAGGTAAAACGGCATTCAATTAGCAAAGAAAACCTCT 1467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1468 TTAGAAAAAGCTCAACCATCAATGTATCAGGCAAAGAAAAAGGCGGACGCGCTATTGTG 1527
                                                                                                                        842 CTTGGCGGTGATGAGCGTGGCGAAGGTAAAAATGGTATTCAATTAGCGAAGAAAACCTCT 901
                                                                                                                                                                                                                                    662 AAAGATAAAAGTGGTAACATTGTTCTCTGCCAAAGAAGGTGAAGCGGAAATTGGCGGT 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 44.6%; Score 2203.8; DB 14; Length 4702; Best Local Similarity 70.7%; Pred. No. 0; Matches 3347; Conservative 0; Mismatches 952; Indels 432; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    688 GIGCAGTTTTACAAGAAAACAACAACTCCGCCGTATTCAACCGTGTTACATCTAACCAA 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              748 ATCTCCCAATTAAAAGGGATTTTAGATTCTAACGGACAAGTCTTTTTAATCAACCCAAAT 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACATITCTAACGAAAACATCAAGGCGCGTAATTTCACCTTCGAGCAAACCAAAGATAAA 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 GACATITCTAACGAAAACATCAAGGCGCGTAATTTCACCCTTGAGCAAACCAAGGATAAA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              928 GCGCTCGCTGAAATTGTGAATCACGGTTTAATTACTGTCGGTAAAGACGGCAGTGTAAAT 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 GCACTCGCTGAAATCGTGAATCACGGTTTAATTACCGTTGGTAAAGACGGTAAAAC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     568 GGAATGGATGTAGTACACGCCACAGCCACTATGCAAGTAGATGGTAATAAAACCATTATC 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           628 CGCAACAGTGTTGACGCTATCATTAATTGGAAACAATTTAACATCGACCAAAATGAAATG 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The isolation and purification of the high molecular weight protein enables the identification of the major protective epitopes of the protein by conventional epitope mapping. These epitopes can then be synthesised using standard techniques and incorporated into fully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GGAATGAGCGTCGTACACGTACAGCATGCAAGTAGACGCCAATAAAACCACTATC 61
                                        /transl_except= AAT encodes Aspartic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                High molecular weight surface proteins – of non-typeable haemophilus which exhibit immunogenic properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4702 BP; 1691 A; 897 C; 944 G; 1170 T; 0 other;
                                                                                                                                                                                                                                                                                                 (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Figure 9; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetic or recombinant vaccines.
                                                                                                                                                                                      93WO-US02166.
                                                                                                                                                                                                                                 92GB-0005704.
misc_difference 983..985
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	TGCTCTTAATCTA 23              TTCTCTTACTTTG 17	-AATAGCAAAGGC 24            AAATTCCCAAGAT 18	7 7	7 7	0 0	71 7	CCATGTTCGCGGC 27	TTCAAATTTCAGC 27                    CTCGAATTTTAGT 22	CATCAATTCAACC 28                  CATTAACTCAAGT 22	CTCAAGCAGCAGC 28 	AGCCAATAACGCC 29	თ — თ	ю 0	TTTTACCAATAAT 31.                     : :CTTTACCAACAAC 25	ю C1	w 0	ო ი —
FTCGCACTGGAACGTCAG		GAGACAGGCGCAAATTTTACCTTTATTAATACATTTCAAGCAATAGCAAAGGC 	TTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGCGTAAATGGCAACATG 	TCATTCAATCTCAAAGAAGGAGGGAAAGTTAATTTCAAATTAAAACCAAACGAGAACAGG 	arcagargaarctitaccaattoggtttttagccaatatcagcagcactggt 	GGGGGCTCTGTTTTTTTATATATATGCCAACCATTCTGGCAGAGGGCTGAGTTAAAA 	angagtgaaattaatatctctaacggcgctaattttaccttaaattcccatgttcgcggc 	GATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCAAATTTCAGC 	CTCAGACAGACGAAAQAIGAITITIAIGACGGGIACGCACGCAAIGCCAICAATICAACC 	TACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAACTCAAGAGAGG 	attacggggaatattactatcgagaagcagcaatgttacgctagaagccaataacgc 	CCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTCGTTAATGG 	AGTTTAAGTTTAACTGGGGAAAATGCAGATATTAAAGGCAATCTCACTATTTCAGAAAGC 	GCCACTITIAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTITACCAATAAT 	- 1 - 8	GATGGTGATTTAAACATTACACTCACGCTAAACGCAACCAAAGAAGCATCATCGGCGGA 	GATATAATCAACAAAAAGGAAGCTTAAATATTACAGACAG
	AACACCTCGTATTGGCAAACCAGCCATGATTCGCACTGGAACGTCAGTGCTCTTAATCT 	GAGACAGGCGCAAATTTTACTTTATTAAATACATTCCAAGC- 	ATAGAAGCTCTGCAGGC                   GTAGAAGTTTTGCAGGG	aagaaggagggaaagti 	CTTTACCAATTCGGTT             AATTACCTATTACTTTT	TTTTGATATATATGCC                  TGTTTGACATACACGCC	ATATCTCTAACGGCGCT                  ACATTACCGGCGCCTT	AAATCAACAAAGACTI! 	GAAAGATGATTTTATGAC            GAAAGATTCTTTTTATAA	TTCTGGCCGTAATGT 	TTACTATCGAGAAGC/ 	ACATAAGGGATAGAGTJ 	CTGGCGAAAATGCAGA)                    CTGGTGCAAATGCAAAA	GAAAGACTAGAGATACC 	CACTGCCGAAATTAATAATAACACAAGGAGTGGTAAAACT 	ACATTACCACTCACGC1 	AACAAAAAGGAAGCTTAAAT
	AACACCTCGTATTO         GATGTTAAATACTO	GAGACAGGCGCAA.          AATACGGTGCAAA.	TTAACAACACAGT,           TTGAGGTCATCAC	TCATTCAATCTCA         AACTTCAACATCG	AACACAAGCAAAC 	GGGGCTCTGTTT           GATAGCTCTGTGA		GATGACGCTTTTA              AGTAATGCTTTTG	CTCAGACAGACGA 	TACAACATATCCA'                CATAATCTAACCA'	ATTACGGGGAATA' 	-	AGTTTAAGTTTAA(             AATTTAAGCCTAA(	8-5		GATGGTGATTTAA              AAAGGTGGTTTAA	GATATAATCAACA
1667	2302	2362	2416	2476	2536 1967	2590	2650	2710	2770	2830	2890	2950	3010	3070	3130 2567	3187	3247
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2687 AATATAACTAACGAAAAAGGCGACTTAAACATCAAGAATATTAAAGCCGACGCCGAAATC 2746 3307 CAAATTGGCGGCAATATCTCGCAAAAGAAGGCAACCTCACGATTTCTTCCGATAAAATT 3366 3367 AATATCACCAAACAGATAACAATCAAAAGGGTATTGATGGAGGAGGACTCTAGTTCAGAT 3426 3427 GCGACAAGTAATGCCAACCTAACTATTAAAACCAAAGAATTGAAATTGACAGAAGACCTA 3486 2867 GAGGCAGAAAATGCTAACCTAACTATTCAAACCAAAGAGTTAAAATTGGCAGGAGCTA 2926 3487 AGTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGTTTAACTATT 3546 3547 GGCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTTAACAATGTT 3606 3607 AAAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACATAAATAGCAAAGTGAAAAAA 3666 3041 AAAGATTCAAAAATCTCGACTGACGGTCACAATGTAACACTAAATAGCGAAGTGAAAACG 3100 3667 TCTAGCAGCAATGGCGGACGTGAAAGCAATAGCGACAACGATACCGGCTTAACTATACT 3726 3101 TCT-----AATGGTAGTAGCAATGCTGGTAATGATAACAGCACCGGTTTAACCATTTCC 3154 3727 GCAAAAAATGTAGAAGTAAACAAAGATATTACTTCTCTCAAAACAGTAAATATCACGC- 3785 3215 GCAGCAGGAAATGTAACAACCAAAGAAGGCACAACTATCAATGCAACCACAGGCAGCGTG 3274 3786 3275 GAAGTAACTGCTCAAAATGGTACAATTAAAGGCAACATTACCTCGCAAAATGTAACAGTG 3334 3335 ACAGCAACAGAAAATCTTGTTACCACAGAGAATGCTGTCATTAATGCAACCAGCGGCACA 3394 3395 GTAAACATTAGTACAAAAACAGGGGATATTAAAGGTGGAATTGAATCAACTTCCGGTAAT 3454 3786 3786 ------GTCGGAAAAGGTTACCACCACAGGCTCGACCATTAACGCAACA 3831 3635 TCCGGCTCTGTAACACTTGTTGCAACTGGAGCAACTCTTGCTGTAGGTAATATTTCAGGT 3694 3889 AACACGGTAAGTGTTAGCGCGACT---GGTGATTTAACCACTAAATCCGGCTCAAAAATT 3945 3695 AACACTGTTACTATTACTGCGGATAGCGGTAAATTAACCTCCACAGTAGGTTCTACAATT 3754 3946 GAAGCGAAATCGGGTGAGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATT 4005 ŏ q Dp õ ò g q οχ g q ŏ g g qq ò qq ŏ ద δ δ q δ ò ò ò ò

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4486 AAGGAAATTGAGGTGAAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGTAATTGAA 4545
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                                                                                                                                                            4366 GCCTCTGGTAGTGTGACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAAC 4425
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                                                                                         1932 CAAACAGGCTCTAGCATTACCTCAAGCAATGGTCAGACACATCTTACAGCCAAGGATAGC 3991
                                                                                                                                                                                                                  4066 GAAATTAATGCGACAGAAGGAGCTGCAACCTTAACCGCAACAGGGAATACCTTGACTACT 4125
                                                  4126 GAAGCCGGTTCTAGCATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGT 4185
                                                                                                                                                                                                      4306 GCTAAGCTAAATGGTGATGCATCAGGTGATAGTACAGAAGTGAATGCAGTCAACGCAAGC 4365
4006 TCCGGTAATACGGTAAATGTTACGGCAAACGCTGGCGATTTAACAGTTGGGAATGGCGCA 4065
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Search completed: March 21, 2003, 21:15:19 Job time: 1049 secs

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March 21, 2003, 20:56:36; search time 156 seconds (without alignments) 9705.533 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/pcTuS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcakfiles1.seq:*
GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                441362 seqs, 153338381 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

C	Description	Sequence 3,	Sequence 3,	Sequence 3,	Sequence 3,	Sednence 3,	Sequence 3,	3, 7	70,	6,	Sequence 6, Appli	9	Sequence 6, Appli	Sequence 6, Appli	o,	Sequence 6, Appli	Sequence 72, Appl	Sequence 1, Appli	٦,	Sequence 1, Appli	1,	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 66, Appl	2,	5,	Sequence 5, Appli
<i></i>		•	<i>\)</i>	' (	2	2	<u>/</u>	_																				
SUMMALES	C a	US-08-038-682-3	-08-302-832-	-530-1	-08-469-8	-08-728	'n	'n	-09-206-942	038-683	02-832	-198	-69	US-08-728-470-6	US-08-617-697-6	US-08-719-641-6	-05	US-08-038-682-1	US-08-302-832-1	US-08-530-198-1	-08-469	-08	-08-617	-08-719-641-	-09-206-942-	-08-038-685-	-08-30	US-08-530-198-5
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æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	97.6	97.6	97.6	97.6	97.6	97.6	97.6	63.0	54.3	54.3	54.3	54.3	54.3		4.	54.3	52.0	52.0	52.0
	Score	4937	4937	4937	4937	4937	4937	4937	4937	4820.2	4820.2	4820.2	4820.2	4820.2	4820.2	4820.2	3108	2680.2	2680.2	2680.2	2680.2	2680.2		2680.2	2680.2	2567	2567	2567
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US-08-469-880-5	US-08-728-470-5	US-08-617-697-5	US-08-719-641-5	US-08-617-697-8	US-08-038-682-8	US-08-302-832-8	US-08-530-198-8	US-08-469-880-8	US-08-728-470-8	US-08-719-641-8	US-08-617-697-7	US-09-206-942-52	US-09-206-942-50	US-09-206-942-46	US-09-206-942-58	US-09-206-942-48	US-09-206-942-60
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9171	9171	9171	9171	4803	4702	4702	4702	4702	4702	4702	4794	2934	2952	3240	2997	3222	2979
52.0	52.0	52.0	52.0	45.5	44.6	44.6	44.6	44.6	44.6	44.6	40.0	32.2	32.2	30.4	30.3	30.1	30.0
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                                                                                        GENERAL INFORMATION:
APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                       ADDRESSE: Shoemaker and Mattare, Ltd
ADDRESSE: Shoemaker and Mattare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bddg. 1
CITY: Arlington
STATE: Willia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                         COUNTY: VIS.A.

ZIP: 22202-0286

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DEAD FLO COMPATIBLE
COMPUTER: DATE NOT NOT STREAM
SOFTWARE: PETENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATE: US-MAR-1993
FILING DATE: 16-MAR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESER; JERRY
REGISTRATION NUMBER: 22.651
REPERENCE/DOCKET UNMER: 1038-293
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4937 base pairs
TYPE: NOTOLOGIC acid
STRANDEDNESS: single
                . Sequence 3, Application US/08038682; Patent No. 5549897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-038-682-3
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Best Local Similarity 100.0
Matches 4937; Conservative
                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
RESULT 1
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9 9	12	18	24.	30.	361	421	481	541	601	661	721	781	841	901	961 961	1021	1081
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1201 GGTAAACTTTCTGCTGATTCTGTAAGCAAAGATAAAAGCGGCAATATTGTTCTTCCGCC 1260
1141 GGCGATATTTTGCCAAAGGCGGTAACATTAATGTCCGTGCTGCCACTATTCGAAACCAA 1200
                                                                             1261 AAAGAGGGTGAAGCGGAAATTGGCGGTGTAATTTCCGCTCAAAATCAGCAAGCTAAAGGC 1320
                                                                                                                                    1261 AAAGAGGTGAAGCGGAAATTGGCGGTGTAATTCCGCTCAAAATCAGCAAGCTAAAGGC 1320
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AGGCAACCTCAC GGGTATTGATGG 	AACCAAAG,               AACCAAAG,	TACAGCCA             TACAGCCA	CGAAGCCA 	CAATGTGA 	TAGCGACA 	TACTTCTC	GACCATTA 	STACGATTT             STACGATTT	SCTCAAAA 	SCGGTACAA               SCGGTACAA	SGAATGGCC                     GAATGGCC	CCTTGACT	CTCAGAAT             CTCAGAAT	GCACCTTA 	TTATTAACGCAAAAGATG 	TCAACGCAAGCGGC 	GGGATT1          GGGATT1
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GAAATTAATATGGC AAAATTAATATCACC 	GATGCGAC               GATGCGAC	CTAAGTAT             CTAAGTAT	ATTGGCAA            ATTGGCAA	GTTAAAGA 	ACATCTAG	ACTGCAAP 	GCGTCGGP	AGTATTAC	ragegegae             ragegegae	SGCTAATG: 	rgttacgg           rgttacgg	GAAGGAGCTGCA 	ATCACTTCAACTAAGGGTC.	ATTAATGCTGCTAATGTG 	TATTAAAG           TATTAAAG	TGCATCAG	TGCGGCAA            TGCGGCAA
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4501 AAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGGAAAAGGCGTCCTT 4560
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5603938-Typeable Haemophilus
NUMBER OF SEQUENCES: 8
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US pct/us93/02166
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/302,832
FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
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FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5603938
GENERAL INFORMATION:
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REGISTRATION NUMBER: 22,651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 1038-404
         TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                   LENGTH: 4937 base pairs
TYPE: nucleic acid
                                                                                        STRANDEDNESS: single
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2881 AGCAGCAGCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCC 2940
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2461 GTAAATGGCAACATGTCATTCAATGTCAAAGAAGGAGGAAAGTTAATTTCAAATTAAAA 2520
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1981 AATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG 2040
                                                                                 GGTTTTTTAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 2100
                                                                                               GATITICAGGGCTAACAACGTATCTITAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 2220
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                                    AATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG 2040
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3001 GTTAATGGGAGTTTAAGTTTAACTGGGGAAAATGCAGATATTAAAGGCAATCTCACTATT 3060
                      3061 TCAGAAAGCGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTTT 3120
                                   3121 ACCAATAATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTT 3180
                                                                                 3181 ACCAATGATGGTGATTTAAACATTACCACTCACGCTAAACGCAACCAAAGAAGCATCATC 3240
                                                                                                                            3301 GAAATCCAAATTGGCGGCAATATCTCGCAAAAAGAAGGCAACCTCACGATTTCTTCCGAT 3360
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                 4201 ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGCTCG 4260
                                                                          4321 GATGCATCAGGTGATAGTACAGAAGTGAATGCAGTCAACGCAAGGGGCTCTGGTAGTGG 4380
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APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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Patent No. 5869065
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                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 4937; DB 2; Length 4937; 100.0%; Pred. No. 0; trive 0; Mismatches 0; Indels 0;
                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                      CURKENT AFPLICATION NUMBER: US/08/530,198
FILING DATE: 13-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
RECISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 22,651
TELECHONE: (703) 415-0813
INFORMATION FOR SEQ ID NO: 3:SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH 4937 base pairs
TYPE: nucleic acid
STRANDENNESS: Single
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100.0
Matches 4937; Conservative
                                                                                                             CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
Virginia
             X: U.S.A. 22202-0286
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US-08-530-198-3
             COUNTRY:
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661 CAATTTAACATCGACCAAAATGAAATGGTGCAGTTTTTACAAGAAAACAACAACTCCGCC 720
                                        721 GTATTCAACCGTGTTACATCTAACCAAATCTCCCAATTAAAAGGGATTTTAGATTCTAAC 780
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821 AATTCAACCTACAACAFATCCATTCTGGGGGTAATGTCACCCTTGGTGGACAAACTC/ 	2881 AGCAGCAGCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCC 	941 AATAACGCCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC 	001 GTTAATGGGAGTTTAAGTTTAACTGGGGAAATGCAGATATTAAAGGCAATCTCACTATT 	081 TCAGAAAGCGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTTT 	121 ACCAATAATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTT 	181 ACCAATGATGATTAAAGATTACCACTCAGGCTAAAGGCAACGAAGAAGGATCATC 	441 GCCGGAGATATAATCAACAAAAAGGAAGCTTAAATATTACAGACAG	001 GAAATCCAAATTGGGGGCAATATCTCGCAAAAAGAAGGAACCTCACGATTTCTTCCGAT 	861 AAAATTAATATCACCAAACAGATAACAATAAAAAGGGTATTGATGAGGGGTCTCTAGT 	12 TCAGATGCGACAAGTAATGCCAACCTATTAAAACCAAAGAATTGAAATTGACAGAA	81 GACCTAAGTATTTCAGGTTTCAATAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTA 	41 ACTATTGGCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTAAC 	01 AATGTTAAAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTG 	61 AAAACATCTAGCAGCAATGGGGGAGGTGAAAGGAATAGCGACAACGATACCGGCTTAACT 	21 ATTACTGCAAAAAATGTAGAAGTAAACAAAGATATTACTTCTCTCAAAACAGTAAATATC 	81 ACCGCGTCGGAAAAGGTTACCACCACAGGGGCTCGACCATTAACGCAACAAATGGCAAA	GCAAGTATTACAACCAAAACAGGTGATATCAGCGGTACGATTTCCGGTAACACGGTAAGT 	
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4621 GCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTTACA 4680
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                                                                      APPLICANT: Barenkamp, Stephen J. TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: Of No. 5876733-Typeable Haemophilus
                                                                                                                                                              ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                         COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/08/469,880
FILING DATE: 06-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1038-516 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JMBER: US PCT/US93/02166
16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/021
FILING DATE: 16-MAR-1993
FILING DATE: 16-MAR-1993
PRIOR APPLICATION NUMBER: US 08/302,832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/302,832 FILING DATE: 16-SEP-1994 ATTORNEY/ABENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION UNBER: 22 651
REGISTRATION UNBER: 22 651
REFERENCE/DOCKET NUBER: 1038
TELEPHONE: (703) 415-0810
TELEPHONE: (703) 415-0813
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4937 base pairs
TYPE: nucleic acid
               Sequence 3, Application US/08469880 Patent No. 5876733 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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                                                                                                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker
                                                                                                                                                                                                                Similarity
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US-08-469-880-3
                                                                          APPLICANT:
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1381 TCAGGTAAAGAAGGGGGAGAACTTACCTTGGCGGTGACGAGGGGGGAAGGTAAAAAC 1440 1381 TCAGGTAAAGAAGGGGGAGAACTTACCTTGGCGGTGACGCGGCGGCGAAGGTAAAAAC 1440 1621 TATTTATCCATTGACAGCAATGCAATTGTTAAAACAAAAGAGTGGTTGCTAGACCCTGAT 1680 1681 GATGTAACAATTGAAGCCGGAAGACCCCTTCGCAATAATACCGGTATAAATGATGATGAATTC 1740 1681 GATGTAACAATTGAAGCCGAAGACCCCTTCGCAATAATACCGGTATAAATGATGATTC 1740 1741 CCAACAGGCACGGTGAAGCAAGGGACCCTAAAAAATAGGGAACTCAAAACAACGCTA 1800 1801 ACCAATACAACTATTTCAAATTATCTGAAAAACGCCTGGACAATGAATATAACGGCATCA 1860 1861 AGAAAACTTACCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATTCTCCAT 1920 1981 AATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTAACGCTTGATCAG 2040 1861 AGAAAACTTACCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATTCTCCAT 1920 1921 AGTAAAGGTCAGCGTGGCGGAGGCGTTCAGATTGATGGAGATATTACTTCTAAAGGCGGA 1980 1981 AATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG 2040 2041 GGTTTTTTAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 2100 2041 GGTTTTTTAAATATTACGGCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 2100 2101 GACGCGCCAAATGCTAAAATTGTCGCCCAGGGCACTGTAACCATTACAGGAGAGGAAAA 2160 2101 GACGCGCAAATGCTAAAATTGTCGCCCAGGCACTGTAACCATTACAGGAGAAAA 2160 GATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 2220 2161 GATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 2220 2221 TCAGTGAATAATTTAACCCACAATCTTAGTGGGCACAATTAACATATCTGGGAATATAACA 2280 2221 TCAGTGAATAATTTAACCCACAAATCTTAGTGGCACAATTAACATATCTGGAATATAAACA 2280 2281 ATTAACCAAACTACGAGAAAGAACACCTCGTATTGGCAAACCAGCCATGATTCGCACTGG 2340 2341 AACGTCAGTGCTCTTAATCTAGAGACAGGCGCAAATTTTACCTTTATTAAATACATTTCA 2400 2161 ò Dp ò qq Db ò Op ò ò g Op ò ò q  $^{0}$ QΩ ò рр qq ò g οp δ ò qq

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252 252 258	2580 2640 2640	2700	2760 2760	2820	2880	2940	3000	3060	3120	3180	3240	3300	3360	3420	3480	3540	3600
TAAAA 11111 TAAAA TCACA	GGGCT 	CCCAT	ATTCA 	CCATC 	ACTCA 	AAGCC	TGCTC	CTATT 	ATTTT        ATTTT	AATGTT        ATGTT	ATCATC	SATGCT	CCGAT	CTAGT 	ACAGAA               ACAGAA	SATTTA 	FTTAAC
TCAAAT 	CCAATA GCAGAG GCAGAG GCAGAG	TAAATI        TAAATI	CAACCA	GCAATG         GCAATG	GACAAA          GACAAA	CGCTAC	GCAGCT         GCAGCT	ATCTC? 	729922 11111	TTGGC2         TTGGC2	GAAGCA	ATAATC        ATAATC	TTTCT	AGGAC	AATTG	GTAGA(	TAACT
TAATT        TAATT	TTTAG	TACCT	PAAATG	ACGCAC	TEGTG	ATGTTA 	AACTTG	AAGGCA        AAGGCA	ATATCA        ATATCA	FAAAAC        FAAAAC	ACCAAA 	ACAGTA        ACAGTA	rcacga        rcacga	ATGGAG 	AATTGA 	AAGATG 	AAACAG
GAAAG1 	TCGGTT CAACCE 	TAATTI        TAATTI	AACCAT            AACCAT	CGGGT/        CGGGT/	CACCCI	AGCAA!        AGCAA!	TATAA        TATAA	TATTAZ        TATTAZ	CCTAA	AGTGG7           AGTGG7	ACGCA! ACGCA!	TACAG	CAACC	aaaattaatatcaccaaacagataacaatcaaaaagggtattgatggagggctctagt 	CAGATGCGACAAGTAATGCCAACCTAACTATTAAAACCAAAGAATTGAAATTGACAGAA 	AGCCA.	GACGGTAACAGCGGTGCCGAAGCCCAAAACAGTAACTTTTAAC
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AAAGAZ 	CCTTTP GATATE        GATATE	TCTAAC         TCTAAC	AACAA           AACAA	GATTT1          GATTT1	66CGG7 	ATCGAC        ATCGAC	AGGGA7               AGGGA7	GAAAAS         GAAAAS	ACTAGI       ACTAGI	ATAACA         ATAACA	ACTCA(	AGCTT	CAAAA	ATCAA	ACTAT	GCAGA         GCAGA	AGCGG
ATCTC 	GCAAA TTTTT 	ATATC        ATATC	AAATC	AAGAT        AAGAT	ATTCTG 	TTACT	ACATA 	ACTGGC ACTGGC	SGAAAG 	TTAAT         TTAAT	ATTACC	AAAGGA 	ATCTCG 	ATAACA 	AACCTA NIIII	AATAAA 	SGTAAC
CATTCA 	ACACAP CTGTTT CTGTTT	AAATTA 	CTTTT	AGACGA            AGACGA	TATCCA                 TATCCA	GGAATA          GGAATA	AGCAAA         AGCAAA	GTTTAA          GTTTAA	TTAAAC         TTAAAC	CCGAAA	TAAAC!	ACAAA!        ACAAA!	GCAATA        GCAATA	AACAGI       AACAGI	ATGCC/        ATGCC/	GTTTCA        GTTTCA	ATGAC
CATGT(           CATGT( CATGA)	CATGA GGGCT       GGGCT	GAGTG	TGACG        TGACG	CAGAC	CAACA	TACGG	TAATC	TTTAA         TTTAA	CACTT	CACTG	TGATT 	AATCA IIII	1166CG	CACCA	AAGTA	TTCAG	GGCAACAGTAAT
GGCAA                 GGCAA   GAGAA	GGGGAA GGTGG IIIII	AAAAT 	GGCGA 	AGCCT AGCCT	AACCTA 	AGCAT	100000	rgggag 	AAGCGC IIIIII	raatgg        raatgg	rgargg 	AGATAT        AGATAT	CCAAAT CCAAAT	FAATAT        FAATAT	rgcgac         rgcgac	AAGTAT          AAGTAT	rggca?
GTAAATGCAACATGTCATTCAATCTCAAAGAAGGAGCGAAAGTTAATTTCAAATTAAAA	CCAAACGAGAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACA GCACTGGTGGGGGCTCTGTTTTTTTGATATATATGCCAACCATTCTGGCAGGGGCT HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GAGTTAAAAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCCCAT 	GTTCGCGGCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCA 	AATTTCAGCTCAGACAGAAGAAGATGATTTTTATGACGGGTACGCACGC	AATTCAACCTACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCA 	AGCAGCACCATTACGGGGAATATTACTATCGAGAAAGCAGCAATGTTACGCTAGAAGCC 	AATAACGCCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC 	GTTAATGGGAGTTTAAGTTTAACTGGGAAAATGCAGATATTAAAGGCAATCTCACTATT 	TCAGAAAGGGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTTT 	ACCAATAATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTT 	ACCAATGATGGTGATTTAAACATTACCACTCACGCTAAACGCAACCAAC	GGCGGAGATATAATCAACAAAAAGGAAGCTTAAATATTACAGACAG	GAAATCCAAATTGGGGGCAATATCTCGCAAAAAGAAGCAACCTCACGATTCTTCCGAT 	AAAAT:       AAAAT:	TCAGA1        TCAGA1	GACCTAAGTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTA 	ACTATT
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4621 GCTGTACGTTTTGTTGAGCCAAATAATACAATTACAGTCAATACACAAAATGAATTTACA 4680
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                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/08728470
Patent No. 5928651
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAILIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
SPLICATION VUMBER: US/08/728,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 08/302,832
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: GB 9205704.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BEKKETESSET, JETTY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-633
TELECOMMUNICATION INFORMATION:
TELEROMONICATION INFORMATION:
TELEROMONE: (703) 415-0813
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4937 base pairs
TYPE: nucleic acid
STRANDENESS: single
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; MOLECULE TYPE: DNA (genomic)
US-08-728-470-3
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ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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US-08-728-470-3
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3181 ACCAATGATGGTGATTTAAACATTACCACTCACGCTAAACGCAACCAAAGAAGATCATC 3240
                      3301 GAAATCCAAATTGGGGGCAATATCTCGCAAAAAGAAGGCAACCTCACGATTTCTTCCGAT 3360
                                                                                                                         3361 AAAATTAATATCACCAAACAGATAACAATCAAAAAGGGTATTGATGGAGAGGACTCTAGT 3420
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                                                          4381 ACTCCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGTTA 4440
                                                                            4501 AAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCCTT 4560
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Sequence 3, Application US/08617697

Sequence 1, Application US/08617697

Sequence 3, Application US/08617697

Sequence 3, Application US/08617697

TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: 0f No. 5977336-Typeable Haemophilus
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2019 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAILS: 2220-0286
ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,697
FILING DATE: 01-APR-1996
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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Virginia
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100.0%; Score 4937; I
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4937; Conservative 0; Mismatches
                                       HILING DATE: 16-MAR-1993
ATTORNEY/AGRIT INFORMATION:
NAME: RAFFATE
                                                                                        NAME: BEKKETESSET, JETTY W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-557
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4937 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
FILING DATE: 05-0CT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/HEOTOMPELING DATE:
                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                               US-08-617-697-3
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                                                              901 TTCACCTTCGAGCAAACCAAAGATAAAGCGCTCGCTGAAATTGTGAATCACGGTTAATT 960
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Qy B	1981	ATAAAAATATACGCTTGATCAG 204
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<u>2</u>	04	GGTTTTTTAAATATTACGCGCTTCCGTAGCTTTTGAAGGGAAATAACAAGCGCC 2100
oy Op	2101	16
oy S	1.6	AACGGAACGGTAAAGGTCTGAATATCATTCA 222
8 8	2161	ATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTC
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Qy Db	2401	AGCAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGC 2460 
δλ	461	TAAATGCAACATGTCATTCAATCTCAAAGAAGGAGCGAAAGTTAATTTCAAATTAAAA 252
QQ	461	CGAAAGTTAATTTCAAA
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Oy Dp	2581 (	CCAACCATTCTGGCAGAGGGGT 264
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g a	761	ANTICAGCCTCAGACCAAAGATGATTTTTATGACGGGTAGCGAGCCAATCCATC 2820 AATTCAGCCTCAGACGAAGAAGATGATTTTATGACGGGTACGCAACGCAATGCCATC 2820
ογ Ph	2821 A	CCTTGGTGGACAAACTCA 288
. A		TAICCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCA 288
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2881 AGCAGCAGCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCC 2940
                            2941 AATAACGCCCCTAATCAGCAAAACATAAGGGATAGATTATAAAACTTGGCAGCTTGCTC 3000
                                               2941 AATAACCCCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAAACTTGGCAGCTTGCTC 3000
                                                                                     3001 GTTAATGGGAGTTTAAGTTTAACTGGGGAAAATGCAGATATTAAAGGCAATCTCACTATT 3060
                                                                                                      3001 GTTAATGGGAGTTTAAGTTTAACTGGCGAAATGCAGATATTAAAGGCAATCTCACTATT 3060
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                                            4381 ACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGTTA 4440
4141 ATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAAGC 4200
                                                                                                       4201 ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGCTCG 4260
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US-08-719-641-3
Sequence 3, Application US/08719641
Fatent No. 6218141
GENERAL INFORMATION:
APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
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TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: Bidg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,641
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1038-625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
YSTEM: PC-DOS/MS-DOS
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NAME: Berkstresse..
NAME: Berkstresse..
REGISTRATION NUMBER: 22.0.2
REFERENCE/DOCKET NUMBER: 1038-cr
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR ESO ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4937 base pairs
... RECIPERISTICS:
... LENGTH: 4937 base pairs
... RECIPERISTICS:
... LENGTH: 4937 base pairs
... RECIPERISTICS:
... RECOMMUNITED:
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                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Matches 4937; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
SOFTWARE: Patent
                                                                                                                                                                                                                                                                                         STATE: Virginia COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                      Arlington
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                                      1561 AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGGAGACATCGGGGCAT 1620
                                                                                           1621 TATTTATCCATTGACAGCAATGCAATTGTTAAAACAAAAGAGTGGTTGCTAGACCCTGAT 1680
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CCACTGGTGGGGGCTCTGTTTTTTGATATATATGCCAACCATTCTGGCAGGGGCT  CCACTGGTGGGGGCTCTGTTTTTTTTTT	TTGGGGGGGGTGAGGGCTTTTAAAATCAACAAGGCTTAACCATAATGCAACCAATTCA TTGGGGGGGGGG	ATTTCAGCCTCAGACAGACGAAAG 	AATICAACCTACAACATATCCATICTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCA 	AGCAC HIII	AATAACGCCCCTAATCAGCAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC 	GTTAATGGGAGTTTAAGTTTAACTGGCGAAAATGCAGATATTAAAGGCAATCTCACTATT 	TCAGAAAGCGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTT 	ACCAATAATGGCACTGCCGAAATTAATATAACACAAGGAGTGGTAAAACTTGGCAATGTT 	ACCAATGATGGTGATTTAAACATTACCACTCACGCTAAACGCAACCAAAGAAGCATCATC 	GGCGGAGATATAATCAACAAAAAAGGAAGCTTAAATATTACAGACAG	GAAATCCAAATTGGGGGCAATATCTCGCAAAAAGAAGGCAACCTCAGGATTCTTCCGAT 	AAAATTAATATCACCAAACAGATAACCATCAAAAGGGTATTGATGGAGGGGCTCTAGT 	TCAGATGCGACAAGTAATGCCAACCTAACTATTAAAACCAAAGAATTGAAATTGACAGAA 	CTAAGTA1 	ACTATTGGCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTAAC 	AATGTTAAAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTG 
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Qy Db	ວາ ວາ	GTTAGCGCGACTGGTGATTTAACCACTAAATCCGGCTCAAAAATTGAAGCGAAATCGGGT 3960 
QY	01 01	61 GAGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGGTA 4020 
QY	4021	0
QY	4081	GAAGGAĞCTGCAACCTTAACCGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCTAGC 4140 
Qy	4141	ATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAAGC 4200
Qy Db	4201	ATTAATGCTGCTAATGTGACATTAAATACTACAGGACCCTTAACCACCGTGGCAGGCTCG 4260 
Qy Db	4261	GATATTAAAGCAACCAGGGGCACCTTGGTTATTAACGCAAAAGATGCTAAGCTAAATGGT 4320
Qy	4321	ю Э
QY	4381	44
QY Db	444]	
oy Dp	4501	951
QY	456	162
OY Db	462	ਵਾਂ ਵਾਂ
QY	468	4 4
Qy	474	1 GGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACAAG 4800

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4801 GTAGATITCATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTACTGTGTGGGTTAAA 4860
                                                     4861 GTTCAGTACGGGCTTTACCCATCTTGTAAAAATTACGGAGAATACAATAAAGTATTTT 4920
                                                                                                           APPLICANT: LOSONOTE, Sheena M.
APPLICANT: LOSONOTE, Sheena M.
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Molecular Weight Proteins
TITLE OF INVENTION NUMBER: US/09/206,942
CURRENT APPLICATION NUMBER: US/09/206,942
EARLIER APPLICATION NUMBER: 09/167,568
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 AATGGTATAATCTTTCATCTTTTAATCTTTCATCTTTCATCTTTCATCTTTCAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 CGGGGTTGTGACCATTCCACAGAAAAGGCTTCCGCTATGTTACTATCTTTAGGTGTAAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 4937; DB 4; Length 4937; 100.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                             Sequence 70, Application US/09206942
Patent No. 6432669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Haemophilus influenzae
                                                                                                                                                                 4921 AACAGGTTATTATTATG 4937
                                                                                                                                                4921 AACAGGTTATTATTG 4937
                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 4937; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                              US-09-206-942-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                             4937
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421 CGGGGTIGTGACCATTCCACAGAAAAGGCTTCCGCTATGTTACTATCTTTAGGTGTAAC 480
                       481 CACTTAGCGTTAAAGCCACTTTCCGCTATGTTACTATCTTTAGGTGTAACATCTATTCCA 540
                                 481 CACTTAGCGTTAAAGCCACTTTCCGCTATGTTACTATCTTTAGGTGTAACATCTATTCCA 540
                                                                    541 CAATCTGTTTTAGCAAGCGGCTTACAAGGAATGGATGTAGTACACGGCACAGCCACTATG 600
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                                                                                  601 CAAGTAGATGGTAATAAAACCATTATCCGCAACAGTGTTGACGCTATCATTAATTGGAAA 660
                                                                                                                              661 CAATTTAACATCGACCAAAATGAAATGGTGCAGTTTTTACAAGAAAACAACAACTCCGCC 720
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AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGGAGACATCGGGGCAT	GATGTAACAATTGAAGCCGAAGACCCCTTCGCAATAATACGGTATAAATGAATT GATGTAACAATTGAAGCGGAAGAACCCCTTCGCAATAATACGGTATAAATGATGAATT GATGTAACAATTGAAGCGAAGAACCCCTTCGGAATAATAACAGGTATAAATACATGATGATGATGATGATGATGATGATGATGATGATGATGA	CCAACAGGCACCGGTGAAGCAAGCGACCCTP 	ACCAATACAACTATTTCAAATTATCTGAAAACGCCTGGACAATGAATATAACGGCATCA 	AGAAAACTTACCGTTAATAGCTCA 	AGTAAAGGTCAGCGTGGCGGAGCGTTCAGATTGATGGAGATATTA 	AATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG 	GGTTTTTTAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAATAACAAAGCACGC 	GACGCGGCAAATGCTAAAATTGTCGCCCAGGGCACTGTAACCATTACAGGAGAGAAAA	1 GATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 	1 TCAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACA 	1 ATTAACCAAACTACGAGAAAGAACACCTCGTATTGGCAAACCAGCCATGATTCGCACTGG	1 AACGTCAGTGCTCTTAATCTAGAGACAGGCGCAAATTTTACCTTTATTAAATACATTTCA 	1 AGCAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCA 	1 GTAAATGGCAACATG; 	1 CCAAACGAGAACATGAACACAAGCAAACCTTTACCAATTCGGTT	1 GCCACTGGTGGGGGCTC 
1561 1561 1621	68		1801	1861	1921 1921	1981 1981	2041	2101	2161	2221	228]	234]	240	246	252	258
6 6 6 6	o vo	Oy Dp	Qy Dp	yo Db	oy Db	Qy Dp	Qy Dp	Qy Dp	δλ	Qy Db	Qy Db	Qy Db	Oy Dp	Oy Op	Qy	QY

70 70 76	- 60 60	2880	4 4	0 0	3060			3240	3300	3360	3420	3480	3540 3540	3600	3660	3720	
41 GAGTTAAAAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCCCAT 2   1   1   1   1   1   1   1   1   1	ATC	TCA	225	1 AATAACGCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC	1 GTTAATGGGAGTTTAAGTTTAACTGGGGAAAATGCAGATATTAAAGGCAATCTCACTATT 3	FTTT 	FGTT           FGTT	CATC	TGCT       TGCT	CGAT        CGAT	TAGT       TAGT	AGAA           AGAA	TTTA	TAAC 1111 TAAC	01 AATGTTAAAGGTTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTG 	4 – A	21 ATTACTGCAAAAAATGTAGAAGTAAACAAAGATATTACTTCTCTCAAAACAGTAAATATC
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                                            3841 GCAAGTATTACAACCAAAACAGGTGATATCAGCGGTACGATTTCCGGTAACACGGTAAGT 3900
                                                                                           3901 GITAGCGCGACTGGTGATTTAACCACTAAATCCGGCTCAAAAATTGAAGCGAAATCGGGT 3960
                                                                                                                                    3961 GAGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGGTA 4020
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                                                                                                                                                                                                                                                                    APPLICANT: BARENRAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PATERLA...
SOFTWARE: PATERLA..
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038,682
                                                                                                                                                                                                                        ; Sequence 6, Application US/08038682
; Patent No. 5549897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                    4921 AACAGGTTATTATTATG 4937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (703) 415-0810
                                                                                                                                      4921 AACAGGTTATTATG 4937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9323 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 98.58 Matches 4864; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                               Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22202-0286
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2341 AACGTCAGTGCTCTTAATCTAGAGACAGGCGCAAATTTTACCTTTATTAAATACATTCA 2400 2401 AGCAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGC 2460 2101 GACGCGGCAAATGCTAAAATTGTCGCCCCAGGGCACTGTAACCATTACAGGAGAGGGAAAA 2160 2161 GATTICAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 2220 1861 AGAAAACTTACCGTTAATAGCTCAATCAACATGGGAAGCAACTCCCCACTTAATTCTCCAT 1920 1921 AGTAAAGGTCAGCGTGGCGGAGGCGTTCAGATTGATGGAGATATTACTTCTAAAGGCGGA 1980 1981 AATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCAG 2040 2041 GGTTTTTAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 2100 2221 TCAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACA 2280 2661 TCAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAAJATAACA 2720 1681 GATGTAACAATTGAAGCCGAAGACCCCCTTCGCAATAATACCGGTATAAATGATGAATTC 1740 1741 CCAACAGGCACCGGTGAAGCAAGCGACCCTAAAAAAAATAGCGAACTCAAAAACAACGCTA 1800 1801 ACCAATACAACTATTTCAAATTATCTGAAAAACGCCTGGACAATGAATATAACGGCATCA 1860 2001 AACGCTCAAGGTAGTGTGATATCGCTAAAACCGGTGGTTTTGTGAGAACTGGGGCAT 2060 2121 GATGTAACAATTGAAGCCGGAAGACCCCCTTCGCAATAATACCGGTATAAATGATGATTC 2180 1501 AAAGAAAAAGGCGGACGCGTATTGTGTGGGGCGATATTGCGTTAATTGACGGCAATATT 1560 1561 AACGCTCAAGGTAGTGGTGATATCGCTAAAACCGGTGGTTTTGTGGAGACATCGGGGCAT 1620 1321 GGCAAGCTGATGATTACAGGCGATAAAGTCACATTAAAAACAGGTGCAGTTATCGACCTT 1380 1381 TCAGGTAAAGAAGGGGGAGAAACTTACCTTGGCGGTGACGAGCGCGGCGAAGGTAAAAAC 1440 1441 GGCATTCAATTAGCAAAGAAAACCTCTTTAGAAAAAGGCTCAACCATCAATGTATCAGGC 1500 2281 ATTAACCAAACTACGAGAAAGAACACCTCGTATTGGCAAACCAGCCATGATTCGCACTGG

ΩP	284	1 AGCAATAGCAAAGGCTTAACAAGTATAGAAGTCTGCAGGGGGTGAATTTTTTTT
ογ	4	1 GTAAATGGCAACATGTCATTCAATCTCAAAGGAGGAAGGTAAGTTAAATTTCAAATTAAAA 2521
Q	σ	1 GTAAATGGCAACATGTCATTCAATCTCAAAGAAGGAGCGAAAGT
S a	252	1 CCAAACGAGAACATGAACACCAAAGCAAACTTTACCAATTCGGTTTTTAGCCAATATCACA 258 
δ	28	1 GCCACIGGIGGGGCTCTGTTTTTTTGATATATGCCAACCATTCTGGCAGGGGCCT 26
g 3	02	. GCCACTGGTGGGGGCTCTGTTTTTTTTTTTTTTTTTTTT
r d	308	1 GAGITAAAATGGGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATCCCAT 2700 
Οy	270]	GCGGCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCA 276
qq	14	ITCGCGGCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCA 320
Qy Dp	3201	AATTICAGCCTCAGACAGACGAAAGAITTITATGACGGGTACGCACGCAATGCCATC 282 
δ	2821	AATTCAACCTACAACATATCCATTGGGGGGGAAAAAAAAA
qq		
οy	2881	AGCAGCAGCATTACGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGTAGAAGC 204
Op	3321	AGCAGCAGCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCC 338
g g	3381	AATAACGCCCCTAATCAGCAAAACATAAGGGATAGACTTATAAAACTTGGCAGCTTGCTC 301
δ	3001	TAATGGGAGTTTAAGTTTAACTGGCGAAAATGCAGATATTAAAGGCAAATGCAAATAAAAATGAAATAATTAAAAGGCAAAATGCAGAAATGCAGAAATAAAT
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ъ с	3561	ACCANTANTIGGACTIGCCGAAATTAATATAACACAAGGACTGGTAAAACTTGGCAATGTT 3180 
ογ	3181	CCAATGGTGATTTAAACATTACCACTCACTCACTCACAAAAAAAA
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٥y	3241	TATAATCAACAAAAAGGAAGCTTAAATATTACAGACAGTAATAATGATGCT 330
QQ	3681	GGGGGGTATATATCAACAAAAAGGAAGCTTAAATATTACAGACAG
δ	3301	CGGCAATATCTCGCAAAAGAAGGCAACCTCACGATTTCTTCCGAT 336
qq	7	AAATCCAAATTGGGGGAATATCTCGCAAAAAGAAGGCAACCTCACGATTTCTTCCGAT 3800
Š f	3361	AAAATTAATATCACCAAACAGATAACAATCAAAAAGGGTATTGATGGAGGAGGACTCTAGT 3420
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οy	3481	CAATAAAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTA 354
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AGATG	AACAG	TACAG:	CTAAA	GATAC	AAAAC	AAAAC	GCAAC	GCAAC	GGTAA	GAAGC	GAAGC	TCCGG	GAAAT	GAAAT	SAAGCC		GCATO	ACCGTG	ACCGTG	CTAAG	CIAAG	GATTT	CAGTA	CAGTA	AGGAA	AGGAA	CGAAAC	AACTTC	AACTTO
GCCAA	GCCAA	GTGAC	GTGAC	GACAAC	ICTCT	ICTCTC	ATTAAC	ATTAAC	ATTIC 	AAATT	AAATT	CAATT	GCGCA	GCGCA	CTACT	ATGGT	ATGGT	TAACC	L I I I I I	AAGATO	שואטאר	ACTGGG	AAACA	AAACA	AGGCA	AGGCA	TGAAG	AGCTA	AGCTA
TTACA	CCGAA	ACAAT	ACAAT	ATAGC 	TTACT	TTACT	CGACC/	2GACC/	TACGA TACGA STACGA	SCTCA?	SCTCA	CGGTA	GAATG	GAATG	CTTGA	TCAGA	TCAGA	CACCT	CACCT	CGCAA	CACACA	IIIII	SGATT	GATT	TTAAG	TTAAG	GTAAT	ACATT	ACATT
CAGAG4	010000	CGGTC	CGGTC	AAGCA	AGATA	AGATA	AGGCT	AGGCT	CAGCG	ATCCG	ATCCG	AATTGC	AGTTGC	AGTTĞ	SAATAC	TTGG	TTGGC	ACAGG	ACAGG	ATTAA	GCAGT	GCAGT	ACTGG	ACTGG(	GTGCG	STGCG	SAAGA!	AGAGA	NGAGA?
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TTCAA	GACGG	ATCTC	ATCTC	99099	BAAGT	SAAGT	ACCACC	CCACC	CAGGT	TAACC	TAACC	CAACA	GCGAT	GCGAT	CCGCA	AGGTA	HIIII AGGTA(	CATTA	CATTA	SCACCI	AGAAG	AGAAG	TGTGA	TGTGA	TAGAA	TAGAA	AGCAA AGCAA	TGATG	TGATG
CAGGI	GTAAT	CAAAA	CAAAA	GCAAT       GCAAT	ATGTA	ATGTA	AGGTT	AGGTT	CCAAA	STGAT	STGATI	CAAGTG	CGCTG	CGCTG	CTTAA	GGGTC	GGGTC	TGTGA	TGTGA	CAGCGC	TAGTAC	TAGTAC	AAGCAC	AAGCAG	AGATGG	GATG	AGGTGT 	TTATC	TTATC
STATI	SCAACA	AGATT	AGATT	TAGCA	AAAA	AAAAA	GGAAA	GGAAA. Tagaa	TACAA	SACTG	SACTG	FGTAAC               FGTAAC	3GCAA4	3GCAA2	GCAAC	ACTAA	ACTAA	GCTAA	GCTAA	GCAAC	GGTGA	GGTGA	ACCTC	ACCTC/	TCGAA!	rcgaa.	ZAGCC/	AAAGAT	AAGAT
CCTAA	PATTG(	rgtta/	GTTA	ACATO	ACTGC	ACTGC	GCGTC	AGTAT	AGTAT	AGCGC	AGCGC	GCTAA 	STTAC	STTAC	SGAGCT IIIIII	ACTTC/	ACTTC?	AATGCT	ATGCI	TTAAA 	CATCA	CATCA	CGGCA	CGGCA	TCATT	TCATT	ATATCO	AAGTA)	AAGTAA
1 GA	1 AC	1 AA	1 AA	1 AA	1 ATT	1 ATT	ACC	מ אני	- GCA	GTT	GIT	GAG GAG	AAT	AAT	GAAC GAAC	ATC/	ATC/	ATTA	ATTA	GATA	GATG	GATG	ACTG	ACTG	AATA	AATA	AAAT       AAAT	GAAA	GAAA
392	354 398	360	404	366.	372	416	3781	3847	4281	3901	4341	3961	4021	4461	4081	4141	4581	4201	4641	4261	4321	4761	4381	4821	4441	4881	4501	4561	5001
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                                                    4681 ACCAGACCGTCAAGTCAAGTGATATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTAAT 4740
                                                                                                   4741 GGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACAAG 4800
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5603938-Typeable Haemophilus
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOHN APPLICATION UNMER: 15-1994

CLASSIFICATION UNMER: US/08/302,832

FILING DATE: 16-SEP-1994

CLASSIFICATION: 435

PRICE APPLICATION: 435
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16-MAR-1993
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
PRIOR APPLICATION NUMBER: GB PCLUS93/021
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-404
TELEPRAN: (703) 415-0813
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9323 DASE pairs
LENGTH: 9323 DASE pairs
TYPE: nucleic acid
STANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                 ; Sequence 6, Application US/08302832; Patent No. 5603938; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                            4921 AACAGGTTATTATTATG 4937
                                                                                                                                                                                                                                                                           5361 AACAGGTTATTATTATG 5377
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
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; MOLECULE TYPE:
US-08-302-832-6
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                                                                                                                                                                                                                                                                                                                                                                        601 CAAGTAGATGGTAATAAAACCATTATCCGCAACAGTGTTGACGCTATCATTAATTGGAAA 660
                                                                                                                                                                                                                                                                                                                                                                                                         421 CGGGGTTGTGACCATTCCACAGAAAAGGCTTCCGCTATGTTACTATCTTTAGGTGTAAC 480
                                                                                                                                                                                                                                                                                   481 CACTTAGCGTTAAAGCCACTTTCCGCTATGTTACTATCTTTAGGTGTAACATCTATTCCA 540
                                                                                                                                   61 CACCTTTTTGCAGTCTATATGCAAATATTTTAAAAAAATAGTATAAAATCGCCATATAA 120
                                                                            121 AATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATCTTTCATCTTTCATCTTTCAT 180
                                                                                                           0; Gaps
                                  Ouery Match
Best Local Similarity 98.5%; Pred. No. 0;
Matches 4864; Conservative 0; Mismatches 73; Indels 0;
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oy Od	102	,
οy	1081	TAATAAACCCAACCATTACAGCATTGCCGCGCCTGAAAATGAAGGGGTCAATT
Q Q	1521	AATAAACCCAACCATTACTTACAGCATTGCCGCGCCTGAAATGAAGGGTCAATCTG 158
δ d	1141	GGCGATATTTTGCCAAAGGCGGTAACATTAATGTCCGTGCTGCTGCTATTCGAAACCAA 1:
3 (	0 0	GGCGATATTTTGCCAAAGGCGGTAACATTAATGTCCGTGCTGCCACTATTCGAAACCAA 1
ž 2	1201	GGTAACTTTCTGCTGATTCTGTAACCAAAGATAAAGGGGCAATATTGTTCTTTCGGCC 1260 
Οy	1261	AAAGAGGTGAAGCGGAAATTGGCGGTGTAATTTCCGCTCAAAATCAAAACCAAAAAAAA
q	1701	
δŏ	1321	GGCAAGCTGATGATTACAGGCGATAAAGTCACATTAAAAACAGGTGCAGTTATCGACCTT 13
qq	1761	GGCAAGCTGATGATAAAGTCCGATAAAGTCACTTAAAAACAGGTGCAGTTATCGACCTT 18
δ,	80	TCAGGTAAAGAAGGGGGAGAAACTTACCTTGGCGGTGACGAGGGCGGGGGAAAAAAC 14
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οy	1681	GAAGCCGAAGACCCCCTTCGCAATAATACCGGTATAAATGATGAATTC 174
qq	2121	ATGTAACAATTGAAGCCGAAGACCCCTTCGCAATAATACCGGTATAAATGATGATTC 218
οy	1741	3AAGCAAGCGACCCTAAAAAAAATAGCGAACTCAAAACAACGCTA 180
Q	2181	CAACAGGCACCGGTGAAGCAAGCGACCCTAAAAAAAATAGCGAACTCAAAACAACGCTA 224
οy	1801	CCAATACAACTATTTCAAATTATCTGAAAAACGCCTGGACAATGAATATAACGGCATC
QQ	2241	CAATACAACTATTTCAAATTATCTGAAAAACGCCTGGACAATGAATATAACGGCATCA 230
οy	1861	GTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATTCTCCA
qq	2301	AAAACTTACCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATTCTCCCAT 236
ογ	21	ATATTACTTCTAAAGGCGGA 198
<b>Q</b> O	61	AAAGGTCAGCGTGGCGGAGGCGTTCAGATTGAT
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2221 TCAGTGAATATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACA 2280 2541 GACGCGGCAAATGCTAAAATTGTCGCCCAGGCACTGTAACCATTACAGGAGAGGGAAA 2600 2161 GATTICAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 2220 2281 ATTAACCAAACTACGAGAAAGAACACCTCGTATTGGCAAACCAGCCATGATTCGCACTGG 2340 2341 AACGICAGIGCICITAAICIAGAGACAGGCGCAAAIITIACCITIAITAAAIACAIITCA 2400 2401 AGCAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGC 2460 2461 GTAAATGGCAACATGTCATTCAATCTCCAAAGAAGGAGGGAAGTTAATTTCAAATTAAAA 2520 2521 CCAAACGAGAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACA 2580 2961 CCAAACGAGAACATGAACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACA 3020 2581 GCCACTGGTGGGGGCTCTGTTTTTTTTGATATATATGCCAACCATTCTGGCAGGGGCT 2640 3021 GCCACTGGTGGGGGGCTCTGTTTTTTTGTATATGCCAACCATTCTGGCAAGGGGCT 3080 2641 GAGTTAAAAATGAGTGAAATTAATATCTCTAACGGCGCTAATTTTACCTTAAATTCCCAT 2700 2701 GTTCGCGGCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCA 2760 2821 AATTCAACCTACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCA 2880 2881 AGCAGCAGTATACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCC 2940 2941 AATAACGCCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC 3000 3001 GTTAATGGGAGTTTAAGTTTAACTGGCGAAAATGCAGATATTAAAGGCAATCTCACTATT 3060 3061 TCAGAAAGCGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTT 3120 3181 ACCAATGATGGTGATTTAAACATTACCACTCAAGGCAACCAAAGAAGGATCATC 3240 ò δ g òγ g δ qq ŏ g ρý οy Dp δy g ŏ q ò g qq ŏ ò q δ g δy q δ qq à Ωp ò à

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                             3981 ACTATTGGCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTTAAC 4040
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3621 ACCAATGATGGTGATTTAAACATTACCACTCACGCTAAACGCAACCAAAGAAGCATCATC 3680
                    3301 GAAATCCAAATTGGCGGCAATATCTCGCAAAAAGAAGGCAACCTCACGATTTCTTCCGAT 3360
                                                                   AAAATTAATATCACCAAACAGATAACAATCAAAAAGGGTATTGATGGAGAGGACTCTAGT 3420
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4321 GATGCATCAGGTGATAGTACAGAAGTGAATGCAGTCAACGCAAGCGGCTCTGGTAGTGTG 4380
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Patent No. S659065
GENERAL INFORMATION:
APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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FILING DATE: 13-DEC-1995
CLASSIFICATION: 424
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IBM PC compatible
:YSTEM: PC-DOS/MS-DOS
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CORRESPONDENCE ADDRESS:
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ZIP: 22202-0286
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                                                                                                                                                                                                                                                                                        97.6%; Score 4820.2; DB 2; Length 9323; 98.5%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                         Pred. No. 0;
0; Mismatches 73; Indels
                                                 REFERENCE/DOCKET NUMBER: JWB-1186
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                 NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                      TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 9323 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-530-198-6
ATTORNEY/AGENT INFORMATION:
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. AGAAAACTTACCGTTAATAGCTCAATCAACATCGGAAGCAACTCCCACTTAATTCTCCA	AGTAAAGGTCAGCGTGGCGGAGGCGTTCAGATTGATGATGAATATTACTTCTAAAGGCGGA 	AATTTAACCATTTATTCTGGCGGATGGGTTGATGTTCATAAAAATATTACGCTTGATCA 	GGTTTTTAAATATTACCGCCGCTTCCGTAGGTTTTGAAGGTGGAAATAACAAAGGCGG 	. GACCCGGCAAATGCTAAAATTGTCGCCCAGGGCACTGTAACCATTACAGGAGAGGGAAAA 	. GATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 	. TCAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACA 	. ATFAACCAAACTACGAGAAAGAACACCTCGTATTGGCAAACCAGCCATGATTCGGACTGG 	. AACGTCAGTGCTCTTAATCTAGAGACAGGGGCAAATTTACCTTTATTAAATACATTTCA 	. AGCAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGC 	. GTAAATGGCAACATGTCATTCAATCTCAAAGAAGGAGCGAAAGTTAATTTCAAATTAAAA 	. CCAAACGAGAACATGAACACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACA 	GCCACTGGTGGGGGCTCTGTTTTTTGATATATATGCCAACCATTCTGGCAGAGGGCT 	GAGTTAAAAATGAGTGAAATTAATATCTCTAACGCGCCTAATTTTACCTTAAATTCCCAT	GTTCGCGGCGATGACGCTTTTAAAATCAACAAAGACTTAACCATAAATGCAACCAATTCA 	AATTTCAGCCTCAGACAAAGATGATTTTTATGACGGGTACGCACGC	AATTCAACCTAGAAATATCCATTCTGGGGGGTAATGTCACCCTTGGTGGAAAACTCA 	AGCAGCAGCATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCC 	AATAACGCCCCTAATCAGCAAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC 
2301	1921	1981 2421	2041	2101	2161	2221	2281	2341	2401	2461	2521	3021	3081	2701 3141	2761 3201	2821 3261	2881 3321	3381
QQ	Qy Dp	Qy Db	Oy Dp	QY Db	Oy Db	Qy Db	Oy Dp	Qy	Qy	Qy Db	QY Db	Qy	Qy Db	Oy Db	Qy Db	Oy Db	Qy Db	Oy Db

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3 (		COGRANDOCCOCCACIIIINAGGGAAAGACIAGGAIACCCIAAAIAICACGGGCAATITT 356
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g ;		CCAATAATGGCACTGCCGAAATTAATAACACAAGGAGTGGTAAAACTTGGCAATGTT 36
Ç,	3181	ACCASTGATGATTAAACATTACCACTCACGCTAAACGCAACGAAGGAGCATCATC 3240
3 ,	9	CCARIGAIGGIGAIITAAACAITACCACICACACAAAAAAAAAA
ολ	24	GGCGGAGATATAATCAACAAAAAGGAAGCTTAAATATTACAGACAG
Op	9	GCGGAGATATAATCAACAAAAAGGAAGCTTAAATATTACAGACAG
οy	30	9
Db	3741	AAATCCAAATTGGCGGCAATATCTCGCAAAAGAAGGCAACCTCACGATTTCTTCCGAT 38
Qy	3361	SATGGAGGACTCTAG
ОÞ	3801	ATATCACCAAACAGATAACAATCAAAAGGGTATTGATGGAGGACTCTAGT 38
Qy	3421	GACAAGTAATGCCAACCTAACTAAAAACCAAAGAATTGAAATTGAC
ρp	3861	CAGATGCGACAAGT
Qy	3481	JTAAGTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTA 354
Dp	3921	98
Qy	3541	3TGCCGAAGCCAAAACGTAACTTTTAAC 360
qq	3981	IATTGGCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTTAAC 404
ογ	3601	CTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTG 366
Dp	4041	STTAAAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTG 410
Qy	3661	ATCTAGCAGCAATGGCGGACGTGAAAGCAATAGCGACAACGATACCGGCTTAACT 3
qq	4101	
Οy	3721	CAAAAAATGTAGAAGTAAAGATATTACTTCTCTCAAAACAGTAAATATC 378
qa	4161	
Qy	3781	CCGCGTCGGAAAAGGTTACCACCACAGCAGGCTCGACCATTAACGCAACAAATGG
QQ	4221	GCGTCGGAAAAGGTTACCACCACAGCGCTCGACCATTAACGCAACAAATGGCAAA 42
Οy	3841	AACACGGTAAGT 390
QQ	4281	CAAGTATTACAACCAAAACAGGTGATATCAGCGGTACGATTTCCGGTAACAGGTAAGT 434
Qy	3901	TAGCGCGACTGGTGATTTAACCACTAAATCCGGCTCAAAAATTGAAGCGAAATCGGGT 396
qq	4341	TTAGCGCGACTGGTGATTTAACCACTAAATCCGGCTCAAAATTGAAGCGAAATCGGGT 4
Qy	3961	AGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGGTA 402
Dp	4401	CTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGGTA 446
Οy	4021	GCGATTTAACAGTTGGGAATGGCGCAGAAATTAATGCGACA 408
Db	4461	STTACGGCAAACGCTGGCGATTTAACAGTTGGGAATGGCGCAGAAATTAATGCGAC

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4081 GAAGGAGCTGCAACCTTAACCGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCTAGC 4140
                     4381 ACTGCGCCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACACTAAATGGGTTA 4440
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                                                                                                                4581 ATCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAAGC 4640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of No. 5876733-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barenkamp, Stephen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08469880 Patent No. 5876733 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GAACGCAAATGATAAAGTAATTTAATTGTTCAACTAACCTTAGGAGAAAATATGAACAAG 360
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                                                                                                                                                        PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038-516 MIS:vg
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,880
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                 US 08/302,832
                                                                                                                                                                                                                                                            APPLICATION NUMBER: GB 9205704.1 FILING DATE: 16-MAR-1992 PRIOR APPLICATION DATA:
                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9323 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 4864; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                        COMPUTER:
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               CITY: P
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B61   CGGGGTTGTGACCATTCCACAGAAAAAGGCAGCGAAAAACCTGCTCGCATGAAAGTGCGT 9	CAATTTAACATCGACCAAAATGAAATGGTGCAGTTTTTA   I	### ### ##############################	AGCGTAAATGGTGGCAGCATTCTTTACTCGCAGGGCAAAAATCACCATCAGCGAT	1201   GGTAAACTTTCTGCTGATTCTGTAAGCAAGATAAAAGCGGCAATATTGTTCTGCCC	1821   TCAGGTAAAGAAGGGGGAGAAACTTACCTTGGCGGTGACGAGCGCGGAAGGTAAAAAC
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CATCGGGGC 	TAGACCCTG	TGATGAAT	AACAACG            AACAACG	TAACGGCATO	AATTCTC              AATTCTC	CTAAAGGCG                CTAAAGGCG	CGCTTGATC 	4 – 4	AGAGGG               AGAGGG	AATATCATT	GGAATATAA(            GGAATATAA	ATTCGCAC' 	AATACATTT            AATACATTT	ATTTTAAC	TCAAATTA 	GCCAATATC           GCCAATATC	GGCAGAGGG                 GGCAGAGGG
TGTGGAGA          TGTGGAGA	STGGTTGC	CGGTATAAA             CGGTATAAA	CGAACTCA.	4 – 4			<b>4</b> – 4	TGAAGGTGGAAATAAC                 TGAAGGTGGAAATAAC	CCATTACAGO 	AAAGGTCTGA 	ACATATCTG               ACATATCTG	CCAGCCATG	CCTTTATTA 	CAGGGGTG2 	AAGTTAAT)              AAGTTAAT)	GGTTTTTAC	ACCATTCT                     ACCATTCT
CGGTGGTTT          CGGTGGTTT	AAAACAAAAGAC 		AAAAAAT 	CGCCTGGAC	4=4	TTGATGGAG2            TTGATGGAG3	TGT 	TTT	SCAC	GAACGGGTA               GAACGGGTA	CAATT	ATTGGCAAA 	CAAATTTTA 	GAAGCTCTG 	aaggagcga             aaggagcga	TACCAATTO               TACCAATTO	TATATGCC           TATATGCC
CGCTAAAAC             CGCTAAAAC	AATTGTT 	CCCCCTT	8-8	¥=¥	AATCAACATCGGA 	5 – 5	ATGGGTT             ATGGGTT	CGTA	GCCCAG 	TTTAAACG	ATCTTAGTG	ACACCTCGT                ACACCTCGT	AGACAGGCG                   AGACAGGCG	CAACACAGTATA 	AATCTCAAAG              AATCTCAAAG	SCAAACCTT                  GCAAACCTT	TTGA
TGGTGATAT          TGGTGATAT	ACAGCAATGC	CGAAC	FGAAGCAAG             FGAAGCAAG		2 – 2	GA – S	TTCTGGCG            TTCTGGCG	922922 	AAAT 	CAACGTAT	AACCCACA!	GAGAAAGAA               GAGAAAGAA	TAATCTAG	AGGCTTAACAACACAGT 	GTCATTCA               GTCATTCA	ACACAP                 ACACAP	GCTCTGTTT'               GCTCTGTTT'
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	3781 ACCGCGTCGGAAAGGTTACCACCACAGCGGGCTCGACCATTAACGCAACAAATGGCAAA 	841 GCAAGTATTACAACCAAAACAGGTGATATCAGCGGTACGATTTCCGGTAACACGGTAACT 	901 GTTAGGGGGACTGGTGATTTAACCACTAAATCGGGCTCAAAAATTGAAGGGAAATGGG 	961 GAGGCTAATGTAACAAGTGCAACAGGTACAAT <sup>†</sup> GGGGGTACAATTTCCGGTAATACGGTA 	021 AATGTTACGGCAAACGCTGGCGATTTAACAGTTGGGAATGGCGCAGAAATTAATGCGAA 	081 GAAGGAGCTGCAACCTTAACGGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCTAGC 	141 ATCACTICAACTAAGGGTCAGGTAGACCICTTGGCTCAGAATGGTAGCATGCAGGAAGC 	201 ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGCGGGCAGGCTGG 	261 GATATTAAAGCAACCAGCGCCACCTTGGTTATTAACGCAAAAGATGCTAAGCTAAATGCT 	21 GATGCATCAGGTGATAGTACAGAAGTGAATGCAGTCA 	381 ACTGCGGCAACCTCAAGCAGTGTGAATATCACTGGGGATTTAAACACAGTAAATGGGTTA 	441 AATATCATTTCGAAAGATGGTAGAAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGGTG 	01 AAATATATCCAGCCAGGTGTAGCAAGTGTAGAAGAAGTAATTGAAGCGAAACGCGTCCTT 	561 GAAAAAGTAAAAGATTTATCTGATGAAGAAAGAGAAACATTAGCTAAACTTGGTGTAAGT 	21 GCTGTACGTTTTGTTGAGCCAANTAATACAATTACAGTGAATACACAAAATGAATTTACA 	81 ACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGAAT 	41 GGC8CACBAGTATGTACCAATGTTGCTGACGATGGACAGCCGTAGTCAGTAATTGACAAG 	01 GTAGATTTCATCCTGCAATGAAGTCATTTTATTTTCGTATTATTTTACTGTGTGGGGTTAAA 
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                                                                                                                                                                                                                           APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                      ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Blidg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US PCT/US93/02166 FILING DARE: 16-MAR-1993
PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGERT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Berkstresser, Jerry W RGISTRATION NUMBER: 2,651
REFERENCE/DOCKET NUMBER: 1038-633
TELECHONE: (703) 415-0810
TELEPHONE: (703) 415-0813
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 923 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LICATION NUMBER: US/08/728,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 08/302,832
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                                                                                                                                                                                    Sequence 6, Application US/08728470 Patent No. 5928651
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER REGARELE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-
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US-08-728-470-6
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                                                                                   4921 AACAGGTTATTATG 4937
                                                                                                 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                               CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LING DATE:
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1021 ATTAGCGTAAATGGTGGCAGCATTTCTTTACTCGCAGGCAAAAAATCACCATCAGCGAT 1080
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                        421 CGGGGTTGTGACCATTCCACAGAAAAGGCTTCCGCTATGTTACTATCTTTAGGTGTAAAC 480
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                                                                                             181 CTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTCATCTTTT 240
                                                                                                                                                                                         241 CACATGAAATGAAGCGGGGAAGGGAGGGAGGGGCAAGAATGAAGAGGGGGCTGAAC 300
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121 AATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATCTTTCATCTTTCATCTTTCAT 180
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272	234	278	240	246	252	302	308	314	320	2821 3261	3321	3381	3001	3061	3121	3181	3241	3301	3361
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4441 AATATCATTTCGAAAGATGGTAGAAACACTGTGCGCTTAAGAGGCAAGGAAATTGAGGTG 4500
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                                         3481 GACCTAAGTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGAGATTTA 3540
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5181 GGCGCACGAGTATGTACCAATGTTGCTGACGATGGACAGCGTAGTCAGTAATTGACAAG 5240
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4621 GCTGTACGTTTTGTTGAGCCAAATAACAATTACAGTCAATACACAAAATGAĀTTTACA 4680
                                                                                                                               4681 ACCAGACCGTCAAGTCAAGTGATAATTTCTGAAGGTAAGGCGTGTTTCTCAAGTGGTAAT 4740
                                                        4561 GAAAAAGTAAAAGATTTATCTGATGAAGAAAGAAAAAAATTAGCTAAACTTGGTGTAAGT 4620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02:
FILING DATE: 16-MAR-100?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22.651
REFERENCE/DOCKET NUMBER: 1038-557
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,697
FILING DATE: 01-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
STATE: Virginia
COUNTR: U.S.A.
ZIP: 22202-0236
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIALE
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08617697 Patent No. 5977336
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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US-08-617-697-6
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    TAAAIAIACAAGAIAAIAAAAAIAAAICAAGAITITIGIGAIGACAAACAACAAITACAA 60

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                                                                                                 97.6%; Score 4820.2; DB 2; Length 9323; 98.5%; Pred. No. 0; tive 0; Mismatches 73; Indels 0;
                                                                                                                           73; Indels
                                                              MOLECULE TYPE: DNA (genomic)
US-08-617-697-6
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                  LENGTH: 9323 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                  Matches 4864; Conservative
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                                                                                                           Similarity
                                         STRANDEDNESS:
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                                                                                                             1081 ATAATAAACCCAACCATTACTTACAGCATTGCCGCGCCTGAAAATGAAGCGGTCAATCTG 1140
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                                                                                                                                                                                                          901 ITCACCITCGAGCAAACCAAAGATAAAGCGCTCGCTGAAAITGTGAATCAGGITTAATT 960
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	GGTTTTTTAAATATTACCGCCGCTTCCGTAGCTTTTGAAGGTGGAAATAACAAAGCACGC 	GACGOGGCAAATGCTAAAATTGTCGCCCAGGCACTGTAACCATTACAGGAGAGGGAAAA 	GATTTCAGGGCTAACAACGTATCTTTAAACGGAACGGGTAAAGGTCTGAATATCATTTCA 	TCAGTGAATAATTTAACCCACAATCTTAGTGGCACAATTAACATATCTGGGAATATAACA 	ATTAACCAAACTAGGAGAAAAAACACCTGGTATTGGCAAACCAGCCATGATTGGAACCTGG 	aacgtcagtgctttattaatctagagacacgcgcaaattttacctttattaaatacatttca 	AGCAATAGCAAAGGCTTAACAACACAGTATAGAAGCTCTGCAGGGGTGAATTTTAACGGC 	GTAAATGGCAACATGTCATTCAATCTCAAAGAAGGAGCGAAAGTTAATTTCAAATTAAAA 	CCAAACGAGAACATGAACAAGCAAACCTTTACCAATTCGGTTTTTAGCCAATATCACA 	GCCACTGGTGGGGCTCTGTTTTTTGATATATGCCAACCATTCTGGCAGAGGGGCT 	GAGTTAAAAATGAGTGAAATTAATATCTCTAACGGGGGCTAATTTTACCTTAAATTCCGAT 	GTTCGCGGCGATGACGCTTTTAAAATCAACAAGACTTAACCATAAATGCAACCAATTCA 		AATTCAACCTACAACATATCCATTCTGGGCGGTAATGTCACCCTTGGTGGACAAAACTCA 	AGCAGCACATTACGGGGAATATTACTATCGAGAAAGCAGCAAATGTTACGCTAGAAGCC 	AATAACGCCCCTAATCAGCAAACATAAGGGATAGAGTTATAAAACTTGGCAGCTTGCTC 	GTTAATGGGAGTTTAAGTTTAACTGGGGAAATGCAGATATTAAAGGCAATGTCACTATT 	TCAGAAAGCGCCACTTTTAAAGGAAAGACTAGAGATACCCTAAATATCACCGGCAATTTT 
2421	2041	2101	2161	2221	2281	2341	2401	2461	2521	3021	3081	3141	3201	3261	3321	3381	3001	3061
Dp	Q <sub>Y</sub>	Qy	Qy Dp	Qy Db	Qy Db	Qy	Qy	Oy Dp	Oy Db	Oy Db	Qy Db	Qy	Qy	Oy Dp	Qy Db	Qy	Qy Dp	δλ

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		CAATAATGGCACTGCCGAAATTAATATAACAAGGAGTGGTAAAACTTGGCAATGT
Oy 3	1181	ACCAATGATGATGATATAAACATTACCACGCTAAACGCAACCAAACAAA
	24	GCGGGGATATAATCAACAAAAAGGAAGCTTAAATATTACAGACGTAATATGATGATGT 3
Db 3	1681	GCGGAGATATAATCAACAAAAAGGAAGCTTAAATATTACAGACAG
Oy 3	3301	GAAATCCAAATTGGCGGCAATATCTCGCAAAAAGAAGGCAACCTCACGATTTCTTCCGAT 33
	361	.T.CACCAAACAGATAAAAAAAAAAAAAAAAAAAAAAAAA
	801	
0y 3	1421	TCAGATGCGACAAGTAATGCCAACCTAACTATAAAACCAAAGAATTGAAATTGACAGAA 34
	48	TAAGTATTTCAGGTTTCAATAAAGCAGAGATTACAGCCAAAGATGGTAGATTTA 3
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Dp 3		CTATTGCCAACAGTAATGACGGTAACAGCGGTGCCGAAGCCAAAACAGTAACTTTTAAC 4
.,	60	AATGTTAAAGATTCAAAAATCTCTGCTGACGGTCACAATGTGACACTAAATAGCAAAGG 36
	04	CTGCTGACGGTCACAATGTGACACTAAATAGCAAAGTG 4
Qy 3 Db 4	3661	AAAACATCTACCAGCAATGGGGGACGTGAAACCAATACGACAACGATACGGCTTAACT 37 
		TACTGCAAAAAATGTAGAAGTAAACAAAGATATTACTTCTCTCAAAACAGTAAATATC 3
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.,	84	GCAAGTATTACAACCAAAACAGGTGATATCAGGGGTACGATTTCGGGTAACACGGTAAGT 3900
Do 4	φ (c	AAGTATTACAACCAAAACAGGTGATATCAGCGGTACGATTTCCGGTAACGGTAAGT 43
QY 3 Db 4	341	GTTAGCGCGACTGGTGATTTAACCACTAAATCGGGCTCAAAAATTGAAGCGAAATCGGGT 3960 
Qy 3	9	AGGCTAATGTAACAAGTGCAACAGGTACAATTGGCGGTACAATTTCCGGTAATACGGTA 40
Db 4	401	
Oy 4	021	GCGATTTAACAGTTGGGAATGGCGCAGAAATTAATGCGACA 40
Db 4	461	STTACGGCAAACGCTGGCCATTTAACAGTTGGGAATGGCGCAGAAATTAATGCGACA 4
Oy 4	8	GAAGGAGCTGCAACCTTAACCGCAACAGGGAATACCTTGACTTGACGCGGTTCTAGC 41
Db 4	521	3AGCTGCAACCTTAACCGCAACAGGGAATACCTTGACTACTGAAGCCGGTTCTAGC 4
2y 4	4	ATCACTICAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGAAGC 420
Db 4	581	TCACTTCAACTAAGGGTCAGGTAGACCTCTTGGCTCAGAATGGTAGCATCGCAGGAAGC 4

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4201 ATTAATGCTGCTAATGTGACATTAAATACTACAGGCACCTTAACCACCGTGGCAGGCTCG 4260
                                                                                                                            4321 GATGCATCAGGTGATAGTACAGAAGTGAATGCAGTCAACGCAAGCGGCTCTGGTAGTGTG 4380
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STRREF: Bldq. 1
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Patent No. 6218141
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MEDIUM TYPE: Floppy disk
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121 AATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATCTTTCATCTTTCAT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.6%; Score 4820.2; DB 4; Length 9323; Best Local Similarity 98.5%; Pred: No. 0; Marches 4864; Conservative 0; Mismatches 73; Indels 0;
            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                         APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1038-625
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                  JMBER: US 08/302,832
16-SEP-1994
                                                                     APPLICATION NUMBER: US/08/719,641
                                                                                                                                                                                                                                                                GB 9205704.1
                                                                                                                                                                                                                                                                                                                         NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // MOLECULE TYPE: DNA (genomic) US-08-719-641-6
                                                                                                                                                                                                                                                                                 FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9323 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: single
                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            FILING DATE: 16-MAR-1
PRIOR APPLICATION DATA:
                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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Db 2061 TATTTAT Qy 1681 GATGTAAN Qy 1681 GATGTAAN Db 2121 GATGTAAN Qy 1741 CCAACAG Db 2181 CCAACAG Qy 1801 ACCAATA	Oy 1861 AGAAAAC Db 2301 AGAAAAC Oy 1921 AGTAAAG Db 2361 AGTAAAG Oy 1981 AATTTAA	Oy 2041 GGTTTTT  Db 2481 GGTTTTT  Oy 2101 GACGCGG  Db 2541 GACGCGG  Oy 2161 GATTCA	2601 2221 2661 2281 2721	Oy 241 AACGTCA Oy 2401 AGCAATA Oy 241 AGCAATA Oy 2461 GTAAATC	Oy 2521 CCAAACG Db 2961 CCACCG Oy 2581 GCCACG Oy 2641 GAGTTAA Oy 2641 GAGTTAA Oy 2670 GTTCGC Oy 2701 GTTCGCC Oy 2711 GTTCGCC
	GGACAAGTCTTTTTAATCCAACCCAAATGGTATCACAATAGGTAAAGACGCAATTAATT	TTCACCTTCGAGCAAACCAAAGTTAAAACGCTGGCTGGCT	1081 ATATAAACCACCATACTTAGGCTGCCCCCCCCGCGCGCGGTCATTGG	1261	GGCATTCAATTAGCAAAGAAAACTCTTTAGAAAAAGGCTCAACCATCAATGTATCAGGC [

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AATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	3 3 3 5 4 5 4 1 C C C C C C C C C C C C C C C C C C
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Search completed: March 22, 2003, 05:46:10 Job time : 258 secs

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March 21, 2003, 20:50:22 ; Search time 6338 Seconds
   (without alignments)
   12615.512 Million cell updates/sec
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                             16154066 seqs, 8097743376 residues
                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                        Scoring table: IDENTITY_NUC Gapoxt 1.0
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em_gss_pro:*
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em_gss_fun:*
em_gss_mam:*
                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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gb_est4:*
gb_est5:*
em_estfun:*
em_estfun:*
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em_gss_inv:*
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em_esthum:*
em_estin:*
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4937
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em_estp::
em_estp::
em_estro:
em_estro:
gb_est::
gb_est2:*
gb_htc:*
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                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                Sequence:
                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES  ID  BH000184 AZ545997 CNS06NAS	)5403 AZ605403 1M0426P11	
DB 17 17 17	17	17
Query Match Length DB 1.6 578 17 1.6 688 17 1.5 403 17 1.5 985 17	625	726
	1.4	7
Score 78.2 76.6 76.6	71.2	707
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Result No. c 1 c 2		

AK018644 Mus muscu	714 Dros	_			AZ549808 ENTFZ62TF	BH478403 BOGJZ72TR	AL436064 T3 end of	PC111-1	AL057797 Drosophil	AL069706 Drosophil	AL052980 Drosophil	AZ676519 ENTGV51TF	AL061936 Drosophil	AL281759 Tetraodon	AL063921 Drosophil	AL253269 Tetraodon	BM274994 PfESToaa7	B12981 T24D11-Sp6	AL097298 Drosophil	AQ922590 RPCI-23-2	AL105023 Drosophil	AZ532642 ENTBP49TR	AL054949 Drosophil		AL075280 Drosophil	AL065999 Drosophil	BE420745 HWM002.B0		AL075432 Drosophil	AL306807 Tetraodon	83	8	AL546530			118	8	AL065764 Drosophil	
AK018644	CNS00LT2	BH834109	AV758661	z	AZ549808	BH478403	CNS07A2Y	AQ347002	CNS00599	CNSOOEVL	CNS0090S	AZ676519	CNS0021J	CNS04AEE	CNS0039G	CNS030F0	BM274994	B12981	CNS00Z6W	AQ922590	CNS0155H	AZ532642	CNS00A5G	BQ876453	CNSOODSU	CNS006W4	BE420745	BH094146	CNSOOITT	CNS04TQ6	AW906883	BG860408	AL546530	BI920072	CNS00Z2B	BM468018	CNS02AH7	CNS006MS	
11	17	17	10	17	17	17	17	17	17	17	17	17	17	17	17	17	13	17	17	17	17	17	17	14	17	17	10	17	17	17	10	12	6	13	17	13	17	17	
1588	1101	490	821	1101	848	372	1063	342	1036	1101	854	951	1101	806	1101	437	265	1223	388	613	1001	855	944	1055	1101	889	1885	420	974	1101	525	570	604	649	1059	1300	417	866	
1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.4	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.3	1.2	1.2	
70.4		on.	O.	68.89	œ	$\sim$	$\sim$	99	99	n	◂	マ	4	ぜ	4	4	4	(7)	m	63.2	(7)	63	63		62.8			62	62	62		61.8							
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## ALIGNMENTS

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plasmid inserts
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gild;4732114|gb|AF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide Kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to
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                                                                                                                                                                                                                                                                                       /lab_host="E. coli strain XLI0-Gold, Tl-resistant, F-"
/hote="Vector: PWD42nv; Purified genomic DNA from M.
musculus C37BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ545997 688 bp DNA linear GSS 14-NOV-200
ENTEB41TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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"I (bases 1 to 688)

Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNN: library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 GTATAAATCCGCCATATAAAATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATCT 161
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                                                                                                                                                                                        /db_xref="texon:10090"
/clone="UUGC2M0287B22"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6%; Score 78.2; DB 17; Length 578; 74.8%; Pred. No. 5.6e-07; Live 0; Mismatches 33; Indels 0.
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Contact: Brendan J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
Institute and Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Plate: 0287 row: B column: 22
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                             /organism="Mus musculus"
                                                                       High quality sequence stop: 578.
Location/Qualifiers
                                                                                                                                                                         /strain="C57BL/6J
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                                                                                                                                                                                                                                                                   /sex="Female"
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Entamoeba histolytica
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hes 98; Conservative
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Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AU034231 403 bp DNA linear GSS 14-DEC-200 IM0528K13F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0528K13 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      128 TAATCTITCATCTITCATCTITAATCTITCATCTITCATCTITCATCTITCATCTITCAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6%; Score 76.6; DB 17; Length 688; 79.1%; Pred. No. 1.3e-06; lve 0; Mismatches 24; Indels 0.
                                                                                                                                                                                                      /organism="Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Std Error: 0.00
                                                                                           Class: shotgun
High quality sequence start: 15
High quality sequence stop: 280.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error
Plate: 0528 row: K column: 13
                                                                                                                                                                                                                            /strain="HM1:IMSS"
/db_xref="taxon:5759"
                                                             DNA library
Seq primer: M13-Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AZ654231.1 GI:11791377
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Fax: 801 585 7177
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Genoscope.

Direct Submission

L Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,

2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:

seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
saccharomyces Kluyveri, Kluyveromyces remracherans, Kluyveromyces
saccharomyces kluyveri, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida troploalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extramities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
Gaillardin, C. and Casaregola, S. Genomic exploration of the hemiascomycetous yeasts: 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Saccharomyces kluyveri"
                                                    Saccharomyces kluyveri
FEBS Lett. 487 (1), 56-60 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:4934"
/clone="AU0AA010G07"
/clone_lib="AU0AA"
/note="end : T3"
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                                                                                                                                                               (bases 1 to 985)
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                                                                                    JOURNAL
                                                                                                                                                                      REFERENCE
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                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 yinch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymorleotide kinase. Adaptor oligonicleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose get of pw72 (gilfy732114)gblAF129072.1), a copy number of pw72 (gilfy732114)gblAF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored for any sheared adaptored mouse DNA was annealed to adaptored for any configuration into adaptored for any configuration into a data selected for ampleillin resistance. "tratagone) cells and selected for amplcillin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNSOGNAS 985 bp DNA linear GSS 17-JUN-200 T3 end of clone AUOAA010G07 of library AUOAA from strain CBS 3082 of Saccharomyces kluyveri, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces kluyveri.
Saccharomyces kluyveri.
Saccharomyces Kluyveri Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 985)
Souchat.J., Aigle.M., Artiguenave.F., Blandin.G.,
                                                                                                                                                                                                                                                                                                                                  /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 985)
Neuveglise,C., Bon,E., Lepingle,A., Wincker,P., Artiguenave,F.,
                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 ITCATCITICATCITIAATCITICATCITICATCITICATCITICATCITICATCITICATCITICA 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="turgclibs18k13"
/clone_lib="mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.5%; Score 76.2; DB 17; Length 403; 79.6%; Pred. No. 1.5e-06; tive 0; Mismatches 23; Indels 0;
         Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 403.
Location/Qualifiers
                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL406538.1 GI:12170669
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CNS06NAS
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                                                                                                 FEATURES
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GSS 13-DEC-2000
                                                                                  re (complement(<857...>808.)

//note="similar to Saccharomyces cerevisiae ORF YOL056w |

GPM3; phosphoglycerate mutase ]"
/evidence=not_experimental
re complement(<860...>985.)
//note="similar to Saccharomyces cerevisiae ORF YDL021w |

GPM2; phosphoglycerate mutase ]"

GPM3; phosphoglycerate mutase ]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ605403 625 bp DNA linear GSS 13-DEC-20G 1M0426P11R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGC1M0426P11 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
/note="similar to Saccharomyces cerevisiae ORF YDL020c (RPN4; 265 proteasome subunit ]"/evidence=not_experimental complement(<857..>985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 TATAATCTTTCATCTTTAATCTTTCATCTTTCATCTTTTCATCTTTCATCTTTCATCTTTC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               1.5%; Score 74.6; DB 17; Length 985; 76.0%; Pred. No. 4e-06; Live 0; Mismatches 29; Indels 0;
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KEYWORDS

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Laboratory Mouse, manaley and the control in the control laboratory mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel clectrophoresis. Vector DNA was prepared from a derivative of pubassis. Vector DNA was prepared from a derivative inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                    Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 625)
Dunn,D., Aoyagil,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Rellly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS 27-APR-2001
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2M0237J15R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0237J15 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4%; Score 71.2; DB 17; Length 625; 75.9%; Pred. No. 2.2e-05; tive 0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plate: 0426 row: P column: 11
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                                                Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  one="UUGC1M0426P11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: plasmid ends
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Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                      plasmid inserts
                                                                                                                                                                                                                                                                                                                                                     USA
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AZ967029
                                                                                                                                                           TITLE
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AZ967029.1 GI:13838256

VERSION

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 Dolymucleotide kinase. Adaptor ollgonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel clectrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil47321141gb) AR129072.1), a copy-number with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically incompanies.
                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 726)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="UUGCZM0237J15"
/clone="tub="mouse 10kb plasmid UUGCZM library"
/sex="Femile=""
/lab_host="E. coli strain XLI0-Gold, Tl-resistant, F-"
/note="vector: PWP42IV: Purified genomic DNA from M:
musculus C575L/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                  Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                         Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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60.4%; Pred. No. 3.4e-05;
Live 0; Mismatches 76; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: 0237 row: J column: 15
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 726.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
Plate: 0237 row: J column: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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Matches 116; Conservative
house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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                      ORGANISM
                                                                                                         REFERENCE
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Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
Garninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
Hara,A., Hayatsu,N., Hill,D., Hirohoka,T., Hori,F.,
Hume,D., Imotani,K., Ishi,Y., Itch,M., Izawa,M., Kasukawa,T.,
Kurihara,C., Matsuyama,T., Myazaki,A., Nishi,K., Nomura,K.,
Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
Schrinl,L., Shibata, Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
Schriml,L., Shibata,Y., Shinagawa,A., Shiraki,T.,
Tanaka,T., Tajama,Y., Tagami,M., Tagawa,A., Takahashi,F.,
Tanaka,T., Tajima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
Hayashiaaki,Y.
                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Ehysical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Gemomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Stangawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 TATAATCITTCATCITTCATCTTTAATCITTCATCITTCATCTTTCATCTTTCATCTTTC 185
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/db_xref="FaNTOM_DB:9130022E09"

/db_xref="MGD:NGI:1997754"

/db_xref="taxon:10090"

/clone="9130022E09"
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/db_xref="MGD:MGI:1921814"
358 c 242 g 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata, K., Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Sumi, V., Ishi, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Pujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayshizaki, Y. Riken integrated sequence analysis (RISA) system - 384-format Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Pormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes conner Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                    HTC 19-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                           Mus musculus adult male cecum cDNA, RIKEN full-length enriched library, clone:9130022E09:unclassifiable transcript, full insert x6016644
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Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
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                                                                                                                                                                                                                                                                                                                                                    AKÖlü644.1 GI:12858457
HTC; CAP trapper
Mus musculus (strain:C578L/6J) adult male cecum cDNA to mRNA,
clone.lib:RKEN full-length enriched mouse cDNA library
clone:9130022E09.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Drosophia Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophia melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophia melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecoral digestion of Drosophila DNA provided by the BDGP from the lisogenic strain y2; on by sp, the same strain used for the BDGP's and bow to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://wacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                        Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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BACPP6-K03.z Pristionchus pacificus BAC ends Pristionchus pacificus
Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophila
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45.0%; Pred. No. 4.4e-05;
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                                               fly), genomic survey sequence.
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Srintvasan, J., Sinz, W., Lanz, C., Brand, A., Nandakumar, R., Raddatz, G., Witte, H., Keller, H., Kipping, I., Pires da Silva, A., Jesse, T., Milare, J., de Both, M., Schuster, S.C. and Sommer, R.J.
A BAC-based genetic linkage map of the nematode Pristionchus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H., Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L.,X.S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and Chen,Z. Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 821)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
T=1: 86-21-50801919(ex.45)
Fax: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV758661 AV Homo sapiens cDNA clone BMFAEF02 5', mRNA sequence.
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Eukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 69.6; DB 17; Length 490; Pred. No. 4.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Pristionchus pacificus BAC ends" 106 c 72 q 201 +
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                                                                                                                                                                                                                          Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pristionchus pacificus"
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Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                              Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="var. California"
/db_xref="taxon:54126"
                        Neodiplogasteridae; Pristionchus.
1 (bases 1 to 490)
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AV758661.1 GI:10916509
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Local Similarity 66.9%;
les 99; Conservative (
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                                                                                                                                                                                                         Contact: Sommer RJ
                                                                                                                                                                                 Unpublished (2002)
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us-10-092-880-3.rst

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Drosophila melanogaster genome survey sequence T7 end of BAC BANIFLL of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Submitted (23-011-1999) Genoscope - Centre National de Sequencage :
Submitted (23-011-1999) Genoscope - Centre National de Sequencage :
Submitted (23-011-1999) Genoscope - Centre National de Sequence for the Bp 191 91006 EVRX cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )
Web : www.genoscope.cns.fr )
Determination of this BAG-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC |
Inbrary (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                              ö
                                /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoletic stem/progenitor cell"
/lab_bost="BMZ5.8"
/note="Vector: yriplEx2; Site_1: sfila; Site_2: sfilB"
139 c 111 g 257 t
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Drosophila malanogaster.
Bukaryota; Metazao, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Epydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                              1.4%; Score 69.6; DB 10; Length 821;
55.1%; Pred. No. 5.3e-05;
tive 0; Mismatches 110; Indels 0;
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/clone="BACN17P12"
/clone_lib="DrosBAC"
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103 c 108 g
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/clone="BMFAEF02"
/clone_lib="BM"
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Matches 135;
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CNS017F7
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ORIGIN

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/Strain="mu:lnss"
//db_rafe="mu:lnss"
//do.me_lib="Entamoba histolytica Sheared DNA"
//clone_lib="Entamoba histolytica Sheared DNA"
//clone_lib="Entamoba histolytica Strain Constructed at The
//note="vector: pH0S1; Site_l: Bst !; Constructed at The
//note="vector: pH0S1; Site_l: Bst !; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond, L.S.
(1993) Entamoba histolytica: a
method for isolate identification. Exp. Parasitol.
//7:450.) The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
the library construction is described in detail in Smith,
the library construction sequencing projects. In Genome
sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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Eukaryota: Entamocbidae; Entamocba.

I (bases 1 to 848)

I oftus, B., Van Aken, S. and Fraser, C.

Inctus, B., Van Aken, S. and Fraser, C.

Inctus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamocba histolytica
HMI: IMSS sheared DNA library

Unpublished (2000)

Contact: Brendan J Loftus

The Institute for Genomic Research

Tel: 301 838 0208

Fax: 301 838 3543

Email: bjloftusetigr.org

Elones are derived from the Entamocba histolytica HMI: IMSS sheared
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ENTFZ62TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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                                                                                                                                                                                                                                                                     113 CCATATAAAATGGTATAATCTTTCATCTTTCATCTTTAATCTTTCATCTTTCATTTTCA 172
                                                  o, Gaps
Match 1.4%; Score 68.8; DB 17; Length 1101; Local Similarity 40.1%; Pred. No. 8.3e-05; hes 109; Conservative 51; Mismatches 112; Indels 0;
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/strain="HM1:IMSS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      910 AAAAAAASSAAAASVRCSSAAASAAAAAAAA 941
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High quality sequence stop: 421.
Location/Qualifiers
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Seg primer: M13-Forward
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Genoscope.
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Best Local Similarity 44.2%
Matches 110; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassica.
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0
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                                                                                                                         68 ITTGCAGTCTATATGCAAATATTTTAAAAAATAGTATAAATCCGCCATATAAAATGGTA 127
                                                                                                                                                                                128 TAATCTITCATCTITCATCTITAATCTITCATCTTTCATCTTTCATCTTTCATCTTTCAT 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="BGGJ"
/rote="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into pHOS1 using BstXI linkers"
59 c 136 g 29 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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Pred. No. 0.00011;
0; Mismatches 103; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
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Pred. No. 0.00013;
0; Mismatches 29; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 372)

Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea Other_GSSs: BOGJZ72TF
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medical Center Drive, Rockville, MD 20850, USA.
                                                                                                                                                                                                                                                                                                                                                                          linear
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/strain="TO1000DH3"
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/clone="BOGJZ72"
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1.4%;
Best Local Similarity 74.6%;
Matches 85; Conservative
    54 c
                                        Query Match 1.4%
Best Local Similarity 55.8%
Matches 130; Conservative
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BH478403/c
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Direct Submitssion

Librated (00-SEP-2000) Genoscope - Centre National de Sequencage,

Z rue Gaston Cremieux, CP 5706, 91057 EWYS cedex - FRANCE (E-mail:

Seqrefégenoscope.cns.fr - Web: www.genoscope.cns.fr)

This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces servazzii, Zygosaccharomyces convaii,

Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces thermotolerans, Kluyveromyces and saccharomyces hansenii var. hansenii, Pithia sorbitophila,

Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of
CNSO7A2Y 1063 bp DNA linear GSS 08-JUL-2001 T3 end of clone BCOAA001B01 of library BCOAA from strain CBS 767 of Debaryomyces hansenii, genomic survey sequence.
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                                                                                                                                                                                                                                                                  Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Debaryomyces.
1 (bases 1 to 1063)
                                                                                                                                                                                                                                                                                                                                                              Souciet, J.L., Aigle, M., Artiguenave, F., Blandin, G., Blandin, G., Bolotin Fukuhara, M., Bon, E., Brottier, P., Casaregola, S., de-Montigny, J., Dujon, B., Durrens, P., Lephigle, A., Llorente, B., Malpertuy, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potler, S., Saurin, W., Tekaia, F., Toffano-Nioche, C., Wesolowski Louvel, M., Mincker, P. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
FEBS Lett. 487 (1), 3-12 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lepingle, A., Casaregola, S., Neuveglise, C., Bon, E., Nguyen, H., Artiguenave, F., Wincker, P. and Gaillardin, C. Genomic exploration of the hemiascomycetous yeasts: 14. Debaryomyces hansenii var. hansenii PEBS Lett. 487 (1), 82-86 (2000)
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14.2%; Pred. No. 0.00015;
Ive 34; Mismatches 105; Indels 0;
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Location/Qualifiers
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/clone="BC0AA001B01"
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                                                                                                                                      AL436064.1 GI:12219477
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100 c 16
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AQ347002 342 bp DNA linear GSS 07-MAY-1999 RPCI11-116J22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-116J22.
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleter@deJong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 342)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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122 AIGGIAIAAICTIICAICTIICAICTIIAAICTIICAICIIICAICTIICAICTIICAICTIICAIC 181
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1.3%; Score 66; DB 17; Length 342
Best Local Similarity 59.7%; Pred. No. 0.00031;
Matches 111; Conservative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850
Fat: 301 838 0200
Fax: 301 838 0208
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/db_xref="GDB:7544397"
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/clone="RPCI-11-116J2"
/clone_lib="RPCI-11"
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                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence.
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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A\_Geneseq\_101001:

A\_Geneseq\_101002:

SIDS1/gcgdata/geneseq\_geneseqp\_embl/AA1980.DAT:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	High molecular wei	Non-typeable Haemo	Haemophilus influe	Haemophilus high m	High molecular wei	Non-typeable Haemo	Haemophilus influe	High molecular wei	High molecular wei	Non-typeable Haemo
SUMMARIES	ID	AAR41724	AAW30294	AAB01848	AAR63506	AAR41728	AAW30292	AAB01849	AAR41723	AAR41732	AAW30293
		14	18	21	15	14	18	21	14	14	18
	Query Match Length DB	1477	1477	1477	1477	1477	1601	1036	1536	1529	1536
di	Query	8.66	99.0	98.0	97.9	97.1	71.3	69.7	67.1	6.99	66.99
	Score	7389	7336	7261	7252	7193	5284	5164	4967	4957	4956
	Result No.	7	7	m	4	S	9	7	89	σ	10

High molecular weight surface proteins - of non-typeable haemophilus which exhibit immunogenic properties

Barenkamp SJ; WPI; 1993-320683/40. N-PSDB; AAQ49507.

PI XX DR DR XX YX PT

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	13		99	1536		AAR41725		High molecular wei
	14	4,	64	1598		AAW30291		Non-typeable haemo
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	17	,	4 4	957		AAB01839		
	18		44	866		AAB01842		
	19		4.4	1079		AAB01836		Haemophilus influe
	20	•		1073		AAB01843		
	22	,	43	975		AAB01826		influ
	23		42	696		AAB01827		
	24	•	40	1011		AAB01832		Haemophilus influe
	52	• •	m 6	1005		AAB01833		Haemophilus influe
	26		20 0	1010		AABU1840 AABU1841		
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	30		3	1095		AAB01835		
	31		36	1227		AAB01824		Haemophilus influe
_	32		3.5	1221		AAB01825		
	33		3.5	1180		AAB01845		
	34		č	1188		AAB01844		
	35		e i	1228		AAB01828		Haemophilus inilue
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	37			320		AABU1829		Amino acid sequenc
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	4 4		_	2411		AAB23860		Haemophilus influe
	42		. •	2353		AAR99393		Haemophilus adhesi
	43			2123		AAE00701		Moraxella catarrha
	4.	489	9.9	3241	23	AAG66005		F. necrophorum leu
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		cope;			ophi	lus influenzae.		
	XX O	Raemonhilus		influenzae.				
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		30-SEP-199	93.					
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	AA PR 1	.6-MAR-1992		92GB-000	-0005704			
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The isolation and purification of the high molecular weight protein enables the identification of the major protective epitopes of the protein by conventional epitope mapping. These epitopes can then be synthesised using standard techniques and incorporated into fully synthetic or recombinant vaccines. Claim 4; Figure 4; 100pp; English.

1477 AA; Sequence

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121 NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180 61 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120 61 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120 181 ARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 240 241 ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 300 301 LSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGE 360 GKNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWGDIALIDGNINAQGSGDIAKTGGFVET 420 421 SGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDEFPTGTGEASDPKKNSELK 480 481 TTLINTISNYLKNAWTMNITASRKLTVNSSINIGSNSHLILHSKGQRGGVQIDGDITS 540 0; Gaps 1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60 541 KGGNLTIYSGGWVDVHKNITLDQGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITG 600 601 EGKDFRANNVSLNGTGKGLNIISSVNNLTHNLSGTINISGNITINQTTRKNTSYWQTSHD 660 SHWNVSALNLETGANFTFIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNF 720 721 KLKPNENMNTSKPLPIRFLANITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTL 780 781 NSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGG 840 Score 7389; DB 14; Length 1477; Pred. No. 0; 0; Mismatches 2; Indels 99.8%; 99.9%; datches 1475; Conservative Local Similarity **Duery Match** 361 199 g ò ò 셤 ð Dp a ò ò g ò g ò g δ g ò g g ð ò à g δ g ò g

961 SIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKEGNLTISSDKINITKQITIKKGIDGE 1020 1021 DSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTV 1080 1081 TENNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKDITSLKT 1140 901 LTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVTNDGDLNITTHAKRNQR 960 1141 VNITASEKVTTTAGSTINATNGKASITTKTGDISGTISGNTVSVSATVDLTKSGSKIEA 1200 1201 KSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEA 1260 GSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVAGSDIKATSGTLVINAKDAK 1320 1321 LNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVNGLNIISKDGRNTVRLRGKE 1380 1381 IEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLGVSAVRFVEPNNTITVNTQN 1440 841 QNSSS\$ITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLVNGSLSLTGENADIKGN 900 Non-typeable Haemophilus; high molecular weight surface protein; Non-typeable Haemophilus high mol.wt. surface protein HMW2. HMW2; hmw2A gene; immunogen; vaccine; otitis media. 1441 EFTTRPSSQVIISEGKACFSSGNGARVCTNVADDGQP 1477 /note= "encoded by TAT" /note= "encoded by ACT" /note= "encoded by TTC" "note= "encoded by CGC" /note= "encoded by GTT" /note= "encoded by ATC" Ą Location/Qualifiers Haemophilus influenzae strain 12. AAW30294 standard; Protein; 1477 14-APR-1998 (first entry) Misc-difference 36 Misc-difference 37 Misc-difference 38 Misc-difference 39 Misc-difference 34 Misc-difference 35 RESULT 2 á g δ 임 ò qq g ά ò ρp ò Q g δ ò g 셤 g õ οy 

/note= "encoded by TTT"

Misc-difference 40

841 QNSSSSITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLVNGSLSLTGENADIKGN 900 

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This protein comprises the high molecular weight surface protein

HWW2 (123 MDa) of non-typeable Haemophilus influenzae strain 12 that

has the immunological ability to protect against disease caused by a

non-typeable Haemophilus strain and is characterised by at least
one surface-exposed B-cell epitope that is recognised by monoclonal

antibody AD6. The HWM2 amino acid sequence was deduced from the

sistuncated, starting at residue 442 of the full-length gene

hmw2 gene sequence (see AAT90995 and AAT90997). The expressed protein

sistuncated, starting at residue 442 of the full-length gene

product. HWW1 (see AAW30291) HWW3 (see AAW30291) and HWW4 (see

C product. HWW1 (see AAW30293), HWW3 (see AAW30292) and Synthetic

peptide of 6-150 amino acids corresponding to at least protective

epitope of HWW2 are also claimed. HWW proteins, conjugates and

c peptides can be used in vaccines, as immunogens for preparation of

antibodies and as antigens for detection of these antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High molecular weight proteins of non-typeable Haemophilus influenzae - useful for vaccine production
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N-PSDB; AAT90995.
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0; Gaps

11; Indels

99.0%; Score 7336; DB 18; Length 1477; 99.2%; Pred. No. 0;

Pred. No. 0; 1; Mismatches

Best\_Local Similarity 99.23 Matches 1465; Conservative

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Query Match

1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60

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1021 DSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTV 1080
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                                          61 SIPQSVLASGLOGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
                                                                                               301 LSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGE 360
                                                                                                                                                                                                                                                                                                            361 GKNGIQLAKKTSLEKGSTINVSCKEKGGFAIVWGDIALIDGNINAQGSGDIAKTGGFVET 420
                            61 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
                                                                                  121 NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180
                                                                                                                                       181 ARNETFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 240
                                                                                                                                                                                             241 ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 300
1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSRYVTIFRCNHLALKPLSAMLLSLGVT 60
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1141 VNITASEKVITTAGSTINATNGKASITTKTGDISGTISGNTVSVSATGDLTTKSGSKIEA 1200
                                                                 1201 KSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEA 1260
                                                                                        1141 VNITASEKVTTTAGSTINATNGKASITTKTGDISGTISGNTVSVSATVDLTTKSGSKIEA 1200
                                                                                                                                        1261 GSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVAGSDIKATSGTLVINAKDAK 1320
                                                                                                                                                           LNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVNGLNIISKDGRNTVRLRGKE 1380
                                                                                                                                                                                                                                1381 IEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLGVSAVRFVEPNNTITVNTQN 1440
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## AAB01848 standard; Protein; 1477 AA

HMW protein; hmw gene; hmwA1; high molecular weight; non-typeable Haemophilus influenzae; NTH1; non-encapsulated; recombinant production; Escherichia coli; antibacterial; vaccine; human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis; Haemophilus influenzae strain 12 HMW2A protein, SEQ ID NO:71. Haemophilus influenzae strain 12. 11-SEP-2000 (first entry) detection; diagnosis. WO200020609-A2, 13-APR-2000. 

98US-0206942 98US-0167568 99WO-CA00938 07-OCT-1999; 07-0CT-1998; 08-DEC-1998;

Loosmore SM, Yang Y, Klein MH; WPI; 2000-303789/26.

(CONN-) CONNAUGHT LAB LTD.

N-PSDB; AAA52197

proteins of Haemophilus which are used as a vaccine to provide protection against Haemophilus induced diseases in humans Example 16; Fig 29A-N; 307pp; English.

Nucleic acid molecule for producing recombinant high molecular weight

influenzae high molecular weight (HMW) proteins in Escherichia coli. The expression construct used to effect recombinant expression comprises a promoter functional in E. coll (e.g., the T7 promoter) operably linked to a modified hwwABC operon from a non-typeable (non-encapsulated) Hillumillumizae (NTHI). Most HMW-expressing NTHI strains contain two hww gene clusters termed hmwlABC and hmwABAC. Each hmwABC operon comprises hmwA, The invention relates to the recombinant production of Haemophilus

proteins which can be used as vaccines to mediate a humoral or cell-mediated immune response to provide protection against diseases in humans caused by H. influenzae (e.g., othits media, epidottitis, proneumonia and tracheobronchitis). The HWM proteins are also useful as antigens in immunoassays for detecting antibodies against Haemophilus, HWW proteins and/or HWW peptides. The nucleotide sequences encoding the HWM proteins can be used to isolate and clone hww genes from other non-typeable strains of Haemophilus via hybridisation reactions. The present sequence represents an HWMA protein from a non-typeable strain of hmwB and hmwC genes. The hmwA genes encode the structural HWWA proteins and the hmwB and hmwC genes encode accessory proteins which are responsible for post-translational processing and secretion of the HWWA proteins. The modified hmwABC operon used in the expression construct of the invention contains an A gene modified such that it encodes only the mature HWMA. The invention also discloses hmwA genes (AAA5175-A52198) and HWMA proteins (AAB01024-B01849) from the non-typeable H. influenzae strains Joyc, KI, K21, LCDC2, PMHJ, 15 and 12. The nucleic acids and vectors are used for the production of recombinant H. influenzae HWM H. influenzae. 9999999999999999999999

## Sequence 1477 AA;

61 9IPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120 Gaps 1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60 ö 98.0%; Score 7261; DB 21; Length 1477; 98.4%; Pred. No. 0; 3; Mismatches 20; Indels Best Local Similarity 98.4 Matches 1454; Conservative Query Match

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181 ARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 240 121 NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180 241 ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 300 ŏ g δ g ò g δλ

301 LSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGE 360 361 GKNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWGDIALIDGNINAQGSGDIAKTGGFVET 420 ρp ŏ g ŏ

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421 SGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDEFPTGTGEASDPKKNSELK 480 481 TTLTNTTISNYLKNAWTMNITASRKLTVNSSINIGSNSHLILHSKGQRGGGVQIDGDITS 540 ö qq δ

541 KGGNLTIYSGGWVDVHKNITLDQGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITG 600 g q ŏ

601 EGKDFRANNVSLNGTGKGLNIISSVNNLTHNLSGTINISGNITINQTTRKNTSYWQTSHD 660 ò q

661 SHWNVSALNLETGANFTFIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNF

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(BARE/) BARENKAMP S J. (SGEM/) ST GEME J W.
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15-MAR-1994;
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             721 KLKPNENMNTSKPLPIRFLANITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTL 780
                                                                       NSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGG 840
                                                                                                                                QNSSSSITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLVNGSLSLTGENADIKGN 900
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61 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
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98.3%; Pred. No. 0;
tive 4; Mismatches
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94WO-US02550
                                             93US-0038682.
                                                                                                                                                                 Barenkamp SJ, St GEME JW;
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TFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKDITSLKT 1140
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SHWNVSALNLETGANFTFIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNF
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                                                                                   LTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVTNDGDLNITTHAKRNQR
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HMW; high molecular weight protein; virus; vaccine; influenza; epitope; immunity; haemophilus influenzae; gene cluster.
                                                                 High molecular weight protein 2 (HMW2).
   AA.
  Protein; 1477
                                            (first entry)
                                                                                                                       Haemophilus influenzae.
  standard;
                                            26-APR-1994
AAR41728
                       AAR41728
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KGGNLTIYSGGWVDVHKNITLDQGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITG 600

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
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                                                                                                                                                                                         High molecular weight surface proteins - of non-typeable haemophilus which exhibit immunogenic properties
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97.1%; Score 7193; DB 14;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1444; Conservative 5; Mismatches 28;
                                                                                             (BARE/) BARENKAMP S J.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                          Claim 4; Figure 4; 100pp; English.
                                                93WO-US02166
                                                                       92GB-0005704
                                                                                                                                                      WPI; 1993-320683/40.
                                                                                                                                                                                                                                                                                                                                               1477 AA;
                                                                                                                                                                   N-PSDB; AAQ49509
                                                                                                                                Barenkamp SJ;
                                               16-MAR-1993;
                                                                       16-MAR-1992;
WO9319090-A
                       30-SEP-1993
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301 LSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGE 360
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541 KGGNLTIYSGGWVDVHKNITLDQGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITG 600
                  601 EGKDFRANNVSLNGTGKGLNIISSVNNLTHNLSGTINISGNITINQTTRKNTSYWQTSHD 660
                          661 SHWNVSALNLETGANFTFIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNF 720
                                                          KLKPNENMNTSKPLPIRFLANITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTL 780
                                                                                            Non-typeable Haemophilus high mol.wt. surface protein HMW4.
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61 SIPOSVLASGLOGMSVVHGTATMQVDGNKTTIRNSVNAIINWKQFNIDQNEMVQFLQESS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This protein comprises the high molecular weight surface protein HWW4 (123 kDa) of non-typeable Haemophilus influenzae strain 5 that has the immunological ability to protect against disease caused by an on-typeable Haemophilus strain and is characterised by at least one surface.exposed B-cell epitope that is recognised by at least one surface.exposed B-cell epitope that is recognised by monoclonal antibody ADG. The HWM4 amino acid sequence was deduced from an isolated hmw4 gene (see AAM79093). HWM1 (see AAM30293), HWM2 (see AAM30294) and HWM3 (see AAM30291) have also been identified. A conjugate comprising HWM4 linked to an antigen, hapten or polysaccharide, and a synthetic peptide of 6-150 amino acids corresponding to at least protective epitope of HWM4 are also claimed. HWM proteins, conjugates and peptides can be used in vaccines, as immunogens for preparation of antibodies and as antigens for detection of these antibodies.
Non-typeable Haemophilus; high molecular weight surface protein; HMW4; immunogen; vaccine; otitis media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Post Local Similarity 68.4%; Pred. No. 3.4e-243;
Matches 1100; Conservative 136; Mismatches 231; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High molecular weight proteins of non-typeable Haemophilus influenzae - useful for vaccine production
                                                                                                                                                                                                     /note= "encoded by TCT"
Misc-difference 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 97-102; 183pp; English.
                                                                                                                                                                 Location/Qualifiers
                                                                                                      Haemophilus influenzae strain 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0617697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-US04707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-503038/46.
N-PSDB; AAT90993.
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qq	301	
QY	361	GKNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWGDIALIDGNINAQGSGDIAKTGGFVET 42.
ò	421	SGHDLFIKDNATVDAKFWII.DFDNVCTNAFDDF ENNWCTNATHDAMAGGS-DIARI'GGFVET 41
o d	ď	
δy	481	LINTIISNYLKNAWTMNITASRKLTVNSSINIGSNSHLILHSKGQRGGGVQIDGDITS 54
qq	480	PILINSTLEQILERGSYVNITANNRIYVNSSINL-SNGSLTLHTKRDGVKINGDITS 53
ò	541	YSGGWVDVHKNITLDQGFLNITAA-SVAFEGGNNKARDAANAKIVAQGTVTI 59
Q	536	VLTIKAGSWVDVHKNITLGTGFLNIVAGDSVAFEREGDKARNATDAQITAQGTITV 59
δλ	599	NNVSLNGTGKGLNIISSVNNLTHNLSGTINISGNITINQTTRKNTSYWQTS 65
QQ	296	
ογ	629	SHWNVSALNLETGANFTFIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGA 71
qq	959	YWNVSSLTLNTVQKFTFIKFVDSGSNSQD
οy	$\leftarrow$	LKPNENMNTSKPLPIRFLANITATGGGSVFFDIYANHSGRGAELKMSEINI
qq	716	ALFKLKPNAATDPKKELPITFNANITATGNSDSSVMFDIHANI
Óγ	775	SHVRGDDAFKINKDLTINATNSNFSLROTKDDFYDGYARNAINSTYNISILGG 83
QQ	776	::
yo d	835	GEN 89
ò	Ò	COLINGO SELLICATATION AND LEGADISNIC CERTETEGNIS VEGNESCE 89
g q	י ס	GNZIJSESATEKOKIKDILALIGNETNNOTAEINITQGVVKL-GNVTNDGDLNITT 95.  GNZIJSESATEKRESININITGREFILI
<b>^</b>	5.4	KRNORSTICCHTINKKOST NITHOGOGININATOLISTICA (1985)
qq	56	
δy	1014	KGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAFTTAKNGDNTTONSNANGT
QQ	1016	
Qy	1074 (	AKTVTFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNK 113
οp	1075	KKYTFDKVKDSKISTDGHNVTLNSEVKTSNGSSNAGNDNSTGLTISAKDVTVNN 113
Οy	34	VNI
QQ	1132	TSHKT
οy	1152	TINATNGKASITTKTGDISGTISGNTVSV
qq	1192	
οy	1190 I	SSKIEAKSGEANVTS
qq	52	TAGSTISATTGNANITTKT
οy	1213 -	NVTANAGDLTVGNGAEINATEGA
QQ	1312 S	TISGNTV
ογ	1248 T	TLTATGNTLTTEAGSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVAGSDIKA 1307                           :

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Mature HMW protein; hmw gene; hmwAl; hmwA2; high molecular weight; non-typeable Haemophilus influenzae; NTH1; non-encapsulated; recombinant production; Escherichia coli; antibacterial; vaccine; human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis;
1372 TLTAESGKLTTQTGSSITSSNGQTTLTAKDSSIAGNINAANVTLNTTGTLTTTGDSKINA 1431
                                     1308 TSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVNGLNIIS 1367
                                                                 1368 KDGRNTVRLRGKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLGVSAVRF 1427
                                                                                                                                               Haemophilus influenzae strain 12 mature HMW2A protein, SEQ ID NO:73.
                                                                                                                                                                                                                              1428 VEPNNTITVNTQNEFTTRPSSQVIISEGKACFSSGNGARVCTNVADDGQ 1476
                                                                                                                                                                                                                                                                                                                                                 AAB01849 standard; Protein; 1036 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                             AAB01849;
                                                                                                                                                                                                                                                                                                            RESULT 7
AAB01849
                                         δλ
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                                                                                                                          δλ
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Haemophilus influenzae strain 12. 98US-0167568. 98US-0206942. 99WO-CA00938. WO200020609-A2. 07-OCT-1999; 07-OCT-1998; 08-DEC-1998; 13-APR-2000.

(CONN-) CONNAUGHT LAB LTD. 

Loosmore SM, Yang Y, Klein MH;

WPI; 2000-303789/26. N-PSDB; AAA52198 Nucleic acid molecule for producing recombinant high molecular weight proteins of Haemophilus which are used as a vaccine to provide protection against Haemophilus induced diseases in humans.

Claim 8; Fig 29E-N; 307pp; English.

The invention relates to the recombinant production of Haemophilus confluenzae high molecular weight (HWW) proteins in Escherichia coli. The expression construct used to effect recombinant expression comprises a promoter functional in E. coli (e.g., the T7 promoter) operably linked to a modified hmwABC operon from a non-typeable (non-encapsulated) H. Clifluenzae (NTHi). Most HWW-expressing NTHI strains contain two hmw gene clusters termed hmwJABC and hmwABC. Each hmwABC operon comprises hmwA, and hmwC genes. The hmwA genes encode accessory proteins which are responsible for post-translational processing and secretion of the HWWA creams encode the structural HWWA proteins creaming and secretion of the HWWA contains and A gene modified such that it encodes only the mature HWWA. The invention also discloses hmwA encodes only the mature HWWA. The invention also discloses hmwA encodes only the capture HWWA. The invention also discloses hmwA encodes only the strains Joyc, KI, KI, LOCZ, PWHI, S and I2. The nucleic acids and vectors are used for the production of recombinant H. influenzae HWW correins which can be used as vaccines to mediate a humoral or cell-mediated immune response to provide protection against diseases in

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humans caused by H. influenzae (e.g., otitis media, epiglottitis, pneumonia and tracheobronchitis). The HWW proteins are also useful as antigens in immunoassays for detecting antibodies against Haemophilus, HWW proteins and/or HWW peptides. The nucleotide sequences encoding the HWW proteins can be used to isolate and clone hmw genes from other non-typeable strains of Haemophilus via hybridisation reactions. The present sequence represents a mature HWWA protein from a non-typeable strain of H. influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1283 SINAANVTLNTTCTLTVAGSDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGS 1342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VKTSSSNGGRESNSDNDTGLTITAKNVEVNKDITSLKTVNITASEKVTTTAGSTINATNG 1162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1163 KASITTKTGDISGTISGNTVSVSATVDLTTKSGSKIEAKSGEANVTSATGTIGGTISGNT 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1223 VNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEAGSSITSTKGQVDLLAQNGSIAG 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AEIQIGGNISQKEGNLTISSDKINITKQITIKKGIDGEDSSSDATSNANLTIKTKELKLT 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTNNGTAEINITQGVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSLNITDSNND 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 623 SSVNNLTHNLSGTINISGNITINQTTRKNTSYWQTSHDSHWNVSALNLETGANFTFIKYI 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFLANI 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 SSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFLANI 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    743 TATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATN 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNFSLROTKDDFYDGYARNAINSTYNISILGGNVTLGGONSSSSITGNITIEKAANVTLE 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       863 ANNAPNQQNIRDRVIKLGSLLVNGSLSLTGENADIKGNLTISESATFKGKTRDTLNITGN 922
                                                                                                                                                                                                                                                                                             443 DNVSINAEDPLFNNTGINDEFPTGTGEASDPKKNSELKTTLTNTTISNYLKNAWTMNITA 502
                                                                                                                                                                                                                                                                                                                                                                         503 SRKLTVNSSINIGSNSHLILHSKGQRGGGVQIDGDITSKGGNLTIYSGGWVDVHKNITLD 562
                                                                                                                                                                                                                                                                                                                                                                                             62 SRKLTVNSSINIGSNSHLILHSKGQRGGGVQIDGDITSKGGNLTIYSGGWVDVHKNITLD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                     563 QGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTGKGLNII 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.7%; Score 5164; DB 21; Length 1036; 99.5%; Pred. No. 1e-237; Live 2; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                1036 AA;
                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                     datches 1030;
                                                                                                                                                                                Sequence
                                                                                                                                                                                                                    Query Match
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                                                                                 121 NSAVENRYTSNQISQLKGILDSNGQVELINPNGITIGKDAIINTNGFTASTLDISNENIK 180
                            1343 VTAATSSSVNITGDLNTVNGLNIISKDGRNTVRLRGKEIEVKYIQPGVASVEEVIEAKRV 1402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 SIPQSVLASGLQCMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
                                            1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
842 SINAANVTLNTTGTLTTVAGSDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGS 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The isolation and purification of the high molecular weight protein enables the identification of the major protective epitopes of the protein by conventional epitope mapping. These epitopes can then be synthesised using standard techniques and incorporated into fully synthetic or recombinant vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
                                                                                                                                                                                                                                                                                                                                                                   HMW; high molecular weight protein; virus; vaccine; influenza; epitope; immunity; haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.1%; Score 4967; DB 14; Length 1536; 67.3%; Pred. No. 3.9e-228; tive 146; Mismatches 264; Indels 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High molecular weight surface proteins - of non-typeable haemophilus which exhibit immunogenic properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BARE/) BARENKAMP S J.
INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                      High molecular weight protein 1 (HMW1).
                                                                                                                                                                                                                                                 AAR41723 standard; Protein; 1536 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Figure 2; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92GB-0005704.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93WO-US02166.
                                                                                                                                                                                                                                                                                                            26-APR-1994 (first entry)
                                                                                                                                                               1022 NGARVCTNVADDGQP 1036
                                                                                                                                              1463 NGARVCTNVADDGQP 1477
                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barenkamp SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9319090-A.
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                                                                                                                                                                                                                                                                               AAR41723;
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a	121	. NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180	
0 y	181	ARNETEEQTKDKALAEIVNHGLITVGKDCSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 24	
9 8	181	ARNETEEQTENDELACIONHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 24	
g q	241		
Qy Dp	301		
Qy Dp	361		
oy Ob	421	SGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDEFPTGTG-BASDPKKNSEL 47 	
O.Y D.b	480	KTTLTNTTISNYLKNAWTWNITASRKLTVNSSINIGSNSHLILHSKGQRGGVQIDGDIT 53 	
λ Q	540		
λς q <sub>Q</sub>	594	9 9	
č q	651 650	NTS-YWQTSHDSHWNVSALNLETGANFTF-IKYISSNSKGLTTQYRSSAGVNFNGVNGNM 70	
Sp 2y	709	SFNLKBGAKVNFKLKPNENMNTSKPLP-IRFLANITATGGGSVFFDIYANHSGRGAE 764    :	
27	765	LKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAIN 824 :  - - -	
ž g	825 825	STYNISILGGNVTLGGONSSSSITGNITIEKAANVTLEANNAPNOONIRDRVIKLGSLLV 884 :     :       :	
& 6	885 883	NGSLSLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGTAEINITGGVVKLGNVT 944 	
7.7 Q0	945	NDGDLNITTHAKRNQRSIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKEGNLTISSDK 1004   : :   :	
λ Q	1005	INITKQITIKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLT 1064 	
λ, q	1065	IGNSNDGNSGAEAKTYTFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTI 1124 	
γ	1125	TAKNVEVNKDITSLKTVNITA-SEKVTTTAGSTINATNGKASITTKT 1170         :      :      ::      ::	
≿ વૃ	1171	VILTATEGALAVSNISGNTVTVTANSGALTTLAGSTIKGTESVTTSSQSGDIGGTISGGT 1241	

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16;
                                                              1302 GSDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVN 1361
1182 VSVSATVDLTTKSGSKIEAKSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEIN 1241
              1362 GLNIISKDGRNTVRLRGKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLG 1421
                                                                                                                                                             The isolation and purification of the high molecular weight protein enables the identification of the major protective epitopes of the protein by conventional epitope mapping. These epitopes can then be synthesised using standard techniques and incorporated into fully synthetic or recombinant vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                              1242 ATEGAATLTATGNTLTTEAGSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVA
                                                                                                                                                                                              Query Match 66.9%; Score 4957; DB 14; Length 1529; Best Local Similarity 67.2%; Pred. No. 1.2e-227; Matches 1033; Conservative 135; Mismatches 227; Indels 142;
                                                                                                                                                                                                                                                                                                                                                                                 HMW; high molecular weight protein; virus; vaccine; influenza; epitope; immunity; haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High molecular weight surface proteins - of non-typeable haemophilus which exhibit immunogenic properties
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NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                           High molecular weight protein 4 (HMW4).
                                                                                                                                                                                                                                                                                 AAR41732 standard; Protein; 1529 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Figure 10; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 93WO-US02166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92GB-0005704.
                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
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(INRM ) INSERM INST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barenkamp SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAR-1992;
                                                                                                                                                                                                                                                                                                                                   26-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9319090-A.
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                                                                                                                                                                                                                                                                                                           AAR41732;
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Qy Dp	133	ISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIKARNFTFGYRDK 1 	192 120
QY Db	193	ALABIVNHGLITVGKDGSVNLIGGKVKNBGVISVNGGSISLLAGQKITISDIINPTITYS ;	252 180
Qy Db	253	IAAPENEAVNLGDIFAKGGNINVRAATIRNOGKLSADSVSKDKSGNIVLSAKEGEAEIGG : 	312 240
Qy Db	313	VISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGEGKNGIQLAKKTS :	372 300
Oy Db	373	LEKGSTINVSGKEKGGFAIVWGDIALIDGNINAQGSGDIAKTGGFVETSGHDLFIKDNAI	432
Qy Db	433	VDAKEWLLDFDWVSINAEDPLFNNTGINDEFPTGTGEASDPKKNSELKTTLTNTTISNYL 1 	492 419
Qy Db	493	KNAWTMNITASRKLTVNSSINIGSNSHLILHSKGQRGGGVQIDGDITS-RGGNLTIYSGG : :    : :     :          :  RRGSYVNITANNRIYVNSSINL-SNGSLTLHTRRDGVKINGDITSNENGNLTIRAGS	551 475
Qy	552	WUDVHKNITLDQGFLNITAA-SVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNV 	610 535
Qy Db	611 536		670
Qy Db.	671 596	ETGANFTFIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENM	728 655
Oy Db	729	NTSKPLPIRFLANITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTLNSHVRG:	786
Qy	787	DDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGGQNSSSS:   :	846
Qy Db	847	ITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLVNGSLSLTGENADIKGNLTISES	906 835
Qy Db	907	ATFKGKTRDTLNITGNFTNNGTAEINITQGVVKL-GNVTNDGDLNITTHAKRNQRSIIGG :	965 895
Qy Dp	966		1025 955
Qy Dp	1026 956	ATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTYTFNNV 	1085
Qy	1086	KDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKDITSLKTVNI	1143
δō	14		9 6
g	1072	AAGNVTTKEGTTINATTGSVEVTAQNGTIKGNITSQNVTV	1131

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1380 EIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLGVSAVRFVEPNNTITVNTQ 1439
                                                                                                                                                                                                                                                                   1320 KLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVNGLNIISKDGRNTVRLRGK 1379
                                                                                                                                                                                                                 1202 SGEANVTSATG-----TIG--- 1215
                                                                   :| ||:|: ||
1192 TGNANITTKTGDINGKVESSSGSVTLVATGATLAVGNISGNTVTITADSGKLTSTVGSTI 1251
                                                                                                  1216 -------GTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTE 1259
                                                                                                              1252 NGTNSVTTSSQSGDIEGTISGNYNVYASTGDLTIGNSAKVEAKNGAATLTAESGKLTTO 1311
                                                                                                                                                    1260 AGSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVAGSDIKATSGTLVINAKDA 1319
                1164 ASITTKTGDISG------TISGNTVSVS------ATVD---LTTKSGSKIEAK 1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This protein comprises the high molecular weight surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-typeable Haemophilus; high molecular weight surface protein; HWM1; hmwlA gene; immunogen; vaccine; otitis media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-typeable Haemophilus high mol.wt. surface protein HMW1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High molecular weight proteins of non-typeable Haemophilus influenzae – useful for vaccine production
                                                                                                                                                                                                                                                                                                        1440 NEFTTRPSSQVIISEGKACFSSGNGARVCTNVADDGQ 1476
                                                                                                                                                                                                                                                                                                                       1492 NEFTTKPSSQVIISEGKACFSSGNGARVCTNVADDGQ 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "encoded by GAT"
Misc-difference 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "encoded by CTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 66-70; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 AAW30293 standard; Protein; 1536 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae strain 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BARE/) BARENKAMP S J.
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HMW1 (125 kDa) of non-typeable Haemophilus influenzae strain 12 that has the immunological ability to protect against disease caused by a non-typeable Haemophilus strain and is characterised by at least on on-typeable Haemophilus strain and is characterised by at least cone sufface-exposed B-cell epitope that is recognised by monoclonal attibuted AD6. The HMW1 amino acid sequence was deduced from the ist truncated, starting at residue 442 of the full-length gene is truncated, starting at residue 442 of the full-length gene product. HMW2 (see AAM30294), HWW3 (see AAM30294), HWW3 (see AAM30294), HWW3 (see AAM30294), HWW3 (see AAM30295) and my30292) have also been identified. A conjugate comprising HWM1 linked to an antigen, hapten or polysaccharide, and a synthetic peptide of 6-150 amino acids corresponding to at least protective peptides can be used in vaccines, as immunogens for preparation of antibodies and as antigens for detection of these antibodies. 8\$888888888888888

1536 AA; Sequence

20; NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120 240 360 GKNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWGDIALIDGNINAQGSGDIAKTGGFVET 420 SGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDEFPTGTG-EASDPKKNSEL 479 Gaps NTS-YWQTSHDSHWNVSALNLETGANFTF-IKYISSNSKGLTTQYRSSAGVNFNGVNGNM 708 1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60 SFNLKEGAKVNFKLKPNENMNTSKPLP-IRFLANITATGGGSVFFDIYANHSG----RGAE 764 **ARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT** LSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGE ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV KTTLTNTTISNYLKNAWTMNITASRKLTVNSSINIGSNSHLILHSKGQRGGGVQIDGDIT ----SKGGNLTIYSGGWVDVHKNITLD-QGFLNITA-ASVAFEGGNNKARDAANAKIVAQ TGDDTRGANLTIYSGGWVDVHKNISLGAQGNINITAKQDIAFEKGSNQV-----ITGQ GTVTITGEGKDFRANNVSLNGTGKGLNIISSVNN---LTHNLSGTINISGNITINQTTRK 98; Length 1536; Indels Query Match 66.9%; Score 4956; DB 18; Best Local Similarity 67.3%; Pred. No. 1.3e-227; Matches 1046; Conservative 146; Mismatches 265; 61 121 61 121 181 181 241 241 361 301 301 421 421 480 479 540 538 591 707 594 651 709 ô g ò 쉽 ò g δ g g ò Q ò δ g ò 셤 ð 엄 δy g qq ò ö a ð g

943 NSKNLSITTNSSSTYRTIISGNITNKNGDLNITNEGSDTEMQIGGDVSQKEGNLTISSDK 1002 1005 INITKQITIKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLT 1064 VSVSATVDLTTKSGSKIEAKSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEIN 1241 1302 GSDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVN 1361 ATEGAATLTATGNTLTTEAGSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVA 1301 : ||: |||:|| : : | ||:|| ||||||| :: | | : || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: || :: LKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAIN 824 INSKYFNVSTGSSLRFKTSGSTKTGFSIEKDLTLNATGGNITLLQVEGT--DGMIGKGIV 824 883 SGNLTAGGNIVNIAGNLTVESNANFKAITNFTENVGGLFDNKGNSNISIAKGGARFKDID 942 STYNISILGGNVTLGGQNSSSSITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLV NGSLSLIGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVT NDGDLNITTHAKRNQRSIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKEGNLIISSDK 1003 INITKQITIKAGVDGENSDSDATNNANLTIKTKELKLTQDLNISGFNKAEITAKDGSDLT 1065 IGNSNDGNSGAEAKTVTFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTI 1063 IGNTNSAD-GTNAKKVTFNQVKDSKISADGHKVTLHSKVETSGSNNNTEHSSDNNAGLTI 1182 VTLTATEGALAVSNISGNTVTANSGALTTLAGSTIKGTESVTTSSQSGDIGGTISGGT LNSSILSCICE------GLNIISKDGRNTVRLRGKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLG High molecular weight protein; HMWI; protective vaccine; otitis; sinusitis; bronchitis; Hib. TAKNVEVNKDITSLKTVNITA-SEKVTTTAGSTINATNGKASITTKT---Haemophilus high molecular weight protein HMW1. AA. AAR63505 standard; Protein; 1536 94WO-US02550 (first entry) 15-MAR-1994; 25-JUN-1995 29-SEP-1994 Haemophilus AAR63505; 885 765 825 945 167 1125 1171 1182 1242 1302 1362 ( RESULT 11 AAR63505 g ŏ g ŏ g Qγ g δ g q qq ò ò ò g ò g ò g ò qq qq å ò 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              594 GTVTITGEGKDFRANNVSLNGTGKGLNIISSVNN---LTHNLSGTINISGNITINQTTRK 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ARNFTFEOTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480 KTTLTNTTISNYLKNAWTMNITASRKLTVNSSINIGSNSHLILHSKGQRGGVQIDGDIT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              540 ----SKGGNLTIYSGGWVDVHKNITLD-QGFLNITA-ASVAFEGGNNKARDAANAKIVAQ 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        538 TGDDTRGANLTIYSGGWVDVHKNISLGAQGNINITAKQDIAFEKGSNQV-----ITGQ 590
                                                                                                                                                                                                                                                                                                                                                                                                                               61 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
                                                                                                                                                                                                   The HWM1 protein encoded by this sequence is useful in a vaccine to protect against disease caused by non-typeable Haemophilus which are not controlled by H. influenzae type b (Hib) vaccines. The encoded protein can also be used as a carrier for protective Hib polysaccharide (in a conjugate vaccin against meningitis) or for other antigens, haptens, etc.
                                                                                                                                                                                                                                                                                                                                                   98; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
                                                                                                                                                                                                                                                                                                                        Query Match 66.7%; Score 4943; DB 15; Length 1536; Best Local Similarity 67.1%; Pred. No. 5.4e-227; Matches 1043; Consery 417; Mismatches 267; Indels 98;
                                                                                                                                        New immunogenic high mol. wt. proteins of non typeable
Haemophilus - useful in protective vaccines
                                                                                                                                                                                Claim 2; Page 31; 127pp; English.
            93US-0038682.
                                                                         Barenkamp SJ, St GEME JW;
                                    (BARE/) BARENKAMP S J. (SGEM/) ST GEME J W.
                                                                                                   WPI; 1994-316665/39.
                                                                                                                                                                                                                                                                                                  1536 AA;
                                                                                                                  Q-PSDB; Q72293
            16-MAR-1993;
                                                                                                                                                                                                                                                                                                   Sequence
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1063 IGNTNSAD-GTNAKKVTFNQVKDSKISADGHKVTLHSKVETSGSNNNTEDSSDNNAGLTI 1121
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651 NTS-YWQTSHDSHWNVSALNLETGANFTF-IKYISSNSKGLTTQYRSSAGVNFNGVNGNM 708
                              767 INSKYENVSTGSSLRFKTSGSTKTGFSIEKDLTLNATGGNITLLQVEGT--DGMIGKGIV 824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB01846 standard; Protein; 1536 AA.
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recombinant production; Escherichia coli, antibacterial; vaccine; human disease; otitis media; epiglottitis; pneumonia; tracheobronchitis;
                                                                                  detection; diagnosis.
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Haemophilus influenzae strain 12

WO200020609-A2.

13-APR-2000

07-OCT-1999;

99WO-CA00938

98US-0167568. 98US-0206942. 07-0CT-1998: 08-DEC-1998;

(CONN-) CONNAUGHT LAB LTD.

Klein MH; Yang Y, Loosmore SM,

WPI; 2000-303789/26. N-PSDB; AAA52195

producing recombinant high molecular weight proteins of Haemophilus which are used as a vaccine to provide protection against Haemophilus induced diseases in humans -Nucleic acid molecule for

Example 16; Fig 28A-Q; 307pp; English.

The invention relates to the recombinant production of Haemophilus influenzae high molecular weight (HMW) proteins in Escherichia coli. The expression construct used to effect recombinant expression comprises a promoter functional in E. coli (e.g., the T7 promoter) operably linked to a modified hmwABC operon from a non-typeable (non-encapsulated) H. Colifluenzae (NTHI). Most HWW-expressing NTHI strains contain two hmw gene clusters termed hmwlaBC and hmw2ABC. Each hmwABC operon comprises hmwA, hmwB and hmwC genes encode accessory proteins which are cresponsible for post-translational processing and secretion of the HWMA proteins. The modified hmwABC operon used in the expression construct of proteins. The modified hmwABC operon used in the expression construct of proteins. The modified hmwABC operon used in the expression construct of mature HWMA. The invention also discloses hmwA genes (AAA72175-A52198) and HWMA proteins and slo discloses hmwA genes (AAA72175-552198) and HWMA proteins discloses hmwA genes (AAA72175-552198) and HWMA proteins which can be used as vaccines to mediate a humoral or proteins which can be used as vaccines to mediate a humoral or cell. mediated immune response to provide protection against Haemophilus, the munical and tracheobronchitis). The HWM proteins are also used to isolate and clone hmw genes from other constructs and present sand presents and human proteins and prot 

1536 AA; Sequence

20; SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120 NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180 Indels 98; Gaps 09 1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT Length 1536; 66.7%; Score 4943; DB 21; ilarity 67.1%; Pred. No. 5.4e-227; Conservative 147; Mismatches 267; Similarity Watches 1043; Query Match Local 61 121 ò g ò g à

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NDGDLNITTHAKRNQRSIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKEGNLTISSDK 1004
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1362 GLNIISKDGRNTVRERGKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLG 1421
1242 VEVKATESLTTQSNSKIKATTGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEIN 1301
                                                                  The isolation and purification of the high molecular weight protein enables the identification of the major protective epitopes of the protein by conventional epitope mapping. These epitopes can then be synthesised using standard techniques and incorporated into fully synthetic or recombinant vaccines. This sequence is claimed to be at the same as that given in AAR41723 (High molecular weight protein although it does differ slightly. (Repeated regions which are possibly incorrect and occur in the corresponding nucleotide coding sequence contribute to these differences).
                                                 1242 ATEGAATLTATGNTLTTEAGSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVA 1301
                                                                                                                1302 GSDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVN 1361
                                                                                                                                                                                                                                              1422 VSAVRFVEPNNTITVNTQNEFTTRPSSQVIISEGKACFSSGNGARVCTNVADDGQ 1476
                                                                                                                                                                                                                                                                   1482 VSAVRFIEPNNTITVDTQNEFATRPLSRIVISEGRACFSNSDGATVCVNIADNGR 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key Location/Qualifiers
Misc-difference 668..677
/note= "Possibly incorrect sequence. Alternative sequence for this region is LNVSESGEFN. (See comments)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HWW; high molecular weight protein; virus; vaccine; influenza; epitope; immunity; haemophilus influenzae; gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High molecular weight surface proteins - of non-typeable haemophilus which exhibit immunogenic properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BARE/) BARENKAMP S J.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              High molecular weight protein 1 (HMW1).
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                                                                                                                                                                                                                                                                                                                                                                 AAR41725 standard; Protein; 1536 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  26-APR-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae.
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1536 AA;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                885 NGSLSLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVT 944
                                                                                                                                                                                                                                                                                                        480 KTTLTNTTISNYLKNAWTMNITASRKLTVNSSINIGSNSHLILHSKGQRGGGVQIDGDIT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                      540 ----SKGGNLTIYSGCWVDVHKNITLD-QGFLNITA-ASVAFEGGNNKARDAANAKIVAQ 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       594 GTVTITGEGKDFRANNVSLNGTGKGLNIISSVNN---LTHNLSGTINISGNITINQTTRK 650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     709 SFNLKEGAKVNFKLKPNENMNTSKPLP-IRFLANITATGGGSVFFDIYANHSG---RGAE 764
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                                                                                                                                            LSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGE 360
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                                                                                                                                                                                                                                                        Ouery Match 66.5%; Score 4924; DB 14; Length 1536;
Best Local Similarity 67.0%; Pred. No. 4.3e-226;
Matches 1042; Conservative 147; Mismatches 268; Indels 98; Gaps
                                                           1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
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1005 INITKQITIKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLT 1064
           1003 INITKQITIKAGVDGENSDSDATNNANLTIKTKELKLTQDLNISGENKAEITAKDGSDLT 1062
                                          IGNSNDGNSGAEAKTVTFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTI 1124
                                                     1182 VSVSATVDLTTKSGSKIEAKSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEIN 1241
                                                                                                                                    -----GDISGTISGNT 1181
                                                                                                                                                                                     1242 ategaatltatgntltteagssitstkgvdllaqngsiagsinaanytlntgtlttva 1301
                                                                                                                                                                                                                                1302 GSDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVN 1361
                                                                                                                                                                                                                                                                         GLNIISKDGRNTVRLRGKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLG 1421
                                                                                                                                                                                                                                                                                                                   1125 TAKNVEVNKDITSLKTVNITA-SEKVTTTAGSTINATNGKASITTKT------
                                                                                                                                                  1182 VTLTATEGALAVSNISGNTVTVTANSGALTTLAGSTIKGTESVTTSSQSGDIGGTISGGT
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                                                                                                                                                                                                                                                                                                                                                              Non-typeable Haemophilus; high molecular weight surface protein; HMM3; immunogen; vaccine; otitis media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-typeable Haemophilus high mol.wt. surface protein HMM3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "encoded by TGT"
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAW30291 standard; Protein; 1598 AA.
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This protein comprises the high molecular weight surface protein than (125 kDa) of non-typeable Haemophilus influenzes strain 5 that has the immunological ability to protect against disease caused by a non-typeable Haemophilus strain and is characterised by at least one surface-exposed B-cell epitope that is recognised by monoclonal solated humwa apene (see AAT90992). HMM1 (see AAW30291), HMM2 (see AAW30294) and HMW4 (see AAW30292), have also been identified. A AAW30294) and HWW4 (see AAW30292) have also been identified. A conjugate comprising HWW3 linked to an antigen, hapten or corresponding to at least protective epitope of fiNW3 are also claimed. HWW proteins, conjugates and peptides can be used in vaccines, as immunogens for preparation of antibodies and as mingens for detection of these antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
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                                                                                                                                                                                                                                                                                                                                                               Matches 1019; Conservative 143; Mismatches 281; Indels 187; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
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                                                                                                                                                                                                                                                                                                                                          DB 18; Length 1598;
   proteins of non-typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1e-217
                                                                                                                                                                                                                                                                                                                                          64.1%; Score 4748.5;
           influenzae - useful for vaccine production
                                           Claim 1; Page 93-97; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                       62.5%;
molecular weight
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1287 ANVTLNTTGTLTTVAGSDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAA 1346
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                                                                                708 -KATFNIAQGSTANFSIK-----ASIMPFKSNANYALFNEDISVSGGGSLNFKLNASS 759
                                                                                                                                                                 759 SG---RGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFY 815
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61 AKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGEGKNGIQLAKKTTLEKGSTIN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 47.6%; Score 3525.5; DB 14; Length 1338; Local Similarity 56.5%; Pred. No. 1.2e-159; es 774; Conservative 136; Mismatches 273; Indels 187; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The isolation and purification of the high molecular weight protein enables the identification of the major protective epitopes of the protein by conventional epitope mapping. These epitopes can then be synthesised using standard techniques and incorporated into fully synthetic or recombinant vaccines.
                                       HMW; high molecular weight protein; virus; vaccine; influenza; epitope; immunity; haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                          High molecular weight surface proteins - of non-typeable haemophilus which exhibit immunogenic properties
                                                                                                                                                                                                                                      (BARE/) BARENKAMP S J.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
          High molecular weight protein 3 (HMW3).
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Figure 10; 100pp; English.
                                                                                                                                                                                                          92GB-0005704.
                                                                                                                                                                              93WO-US02166
                                                                                     Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ49510.
                                                                                                                                                                                                                                                                                     Barenkamp SJ;
                                                                                                                                                                            16-MAR-1993;
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                                                                                                                                               30-SEP-1993.
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6 ENWNTSKPLPIRFLANITATGGSVFFDIYANHSGRGAELKMSEINISNG : :   :	6 ANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGN	6 VTLGGQNSSSSITGNITIEKAANVTLE-ANNAPNQQNIRDRVIKLGSLLVNGSLSLTG 	3 ENADIKGNLTISESATFKGKTRDŢLNITGNFTNNGTAEINITOGVVKLGNVTNDGDLNIT 	3 THAKRNORSIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKEGNLTISSDKINITKQIT 	3 IKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKABITAKDGRDLTIGNSNDGN 	SGAEAKTVTFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESN.  -  -  -  -  - -	KDITSLKTVNITASEKVT	TTAGSTINATNCKASITTKTGDISGTISGNTVSVS-    :     :	-LTTKSGSKIEAKSGEANVTSATG	DSG	ATLTATGNTLTTEAGSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVAGSDIK 	ATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVNC 	SKDGRNTVRLRCKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLGVSAVR  ::	EVEPNNITIVNIQNEFTIRPSSQVIISEGKACFSSGNGARVCTNVADDGQ 1476 
72(	77(	836 578	632	953	1013	1073	1133	1151	1190 988	1213	1247	1307	1367	1427
Qy Dp	Oy Dp	Q <sub>y</sub>	Qy Dp	OY.	Qy Db	oy da	Qy	Qy Dp	Qy Dp	Oy Dp	Qy Dp	Qy Db	Oy Dp	QY

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                                                            March 24, 2003, 15:24:19; Search time 18 Seconds (without alignments) 2414.314 Million cell updates/sec
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                                                                                                                  1 MNKIYRLKFSKRLNALVAVS......CFSSGNGARVCTNVADDGOP 1477
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                                                                                                                                                                                                                                                              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                              262574 segs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Ouery Match
100.0%; Score 7407; DB 1; Length 1477;
DB 15. Length 1477;
100.0%; Pred. No. 0;
Matches 1477; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: 8
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CORRESPONDENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: 8
COURTY: 10.00 To ferson Davis Hwy., 1203 Crystal Plaza
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: 10.00 To ferson Davis Hwy., 1203 Crystal Plaza
STATE: 10.00 To ferson Davis Hwy., 1203 CORPUTER
CONTRY: 0.5.A.

ZIP: 22202-0286
COMPUTER READABLE FORM: PC-DOS/MS-DOS
SOFTWARE: 18M PC Compatible
COMPUTER: 18M PC COMPATIBLE
COMPAT
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BARBAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HARMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
ALIGNMENTS
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTATION UNDHER: 22.651
REFERENCE/COCKET NOMBER: 1038-
TELECOMMUNICATION INFORMATION:
                                                                                                                                           RESULT 1
US-08-038-682-4
; Sequence 4, Application US/08038682
; Patent No. 5549897
; GENERAL INFORMATION:
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TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-08-038-682-4
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Appl Appl Appl Appli Appli

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Sequence Sequence Sequence

US-08-719-641-9 US-09-206-942-51 US-09-206-942-53 US-09-206-942-59 US-09-206-942-59

4751.5 3525.5 3525.5 3396.5 3365.5 3260.3

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

120	180	240	300	360	420	480	540	009	099	720	780	840	006	096	1020	1080	1140
SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 	NSAVENRYTSNQISOLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 	. ARNFTFEOTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 	. ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 	. LSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGE 	. GKNGIQLAKKTSLEKGSTINVSGKEKGGFALVWGDIALIDGNINAQGSGDIAKTGGFVET 	SGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDEFPTGTGEASDPKKNSELK 	TTLTNTTISNYLKNAWTMNITASRKLTVNSSINIGSNSHLILHSKGGRGGVQIDGDITS 	KGGNLTIYSGGWVDVHKNITLDQGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITG 	EGKDFRANNVSLNGTGKGLNIISSVNNLTHNLSGTINISGNITINQTTRKNTSYMQTSHD 	SHWNVSALMLETGANFTETKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNF 	KLKPNENMMTSKPLPIRELANITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTL 	NSHVRGDDAFKINKDLTINATUSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGG 	ONSSSSITGNITIEKAANVTLEANNAPNOONIRPRVIKLGSLLVNGSLSLTGENADIKGN 	LTISESATFKGKTRDTLNITGNFTNNGTAEINITGGVVKLGNVTNDGDLNITTHAKRNQR 	SIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKEGNLTISSDKINITKQITIKKGIDGE 	DSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTV 	TFNNVKDSKISADGHNYTLNSKVKTSSSNGGRESNSDNDTGLFITAKNVEVNKDITSLKT 
61	121	181	241	301	361	421	481	541	601	661	721	781	841	901	961	1021	1081
QV QD	Qy Dp	Qy Dp	Qy Dp	Qy Dp	Oy Dp	Qy	Oy Op	QY Db	Qy Dp	Qy Dp	Qy Dp	Qy Dp	oy Op	6 6y	oy Oy	0y Dp	Qy Db

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1141 VNITASEKVTTTAGSTINATNGKASITTKTGDISGTISGNTVSVSATVDLTTKSGSKIEA 1200
                      1141 VNITASEKVTTTAGSTINATNGKASITTKTGDISGTISGNTVSVSATVDLTTKSGSKIEA 1200
                                                                                                        1201 KSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEA 1260
                                                                                                                                                                                        1261 GSSITSTKGQVDLLAQNGSIAGSINAANVTLNTGTLTTVAGSDIKATSGTLVINAKDAK 1320
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                                                                                    KSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEA 1260
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5603938-Typeable Haemophilus
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza STREET: Bidg. 1
CITY: ArLington
STATE: Virginia
COUNTR: U.S.A.
ZIP: Z2202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                               EFTTRPSSQVIISEGKACFSSGNGARVCTNVADDGQP 1477
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/302,832
FILING DATE: 16-SEP-1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 16-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1038-404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08302832 Patent No. 5603938 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Berkstresser, Jerry W
REGISTRATION UNDBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
FELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
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100.0%; Score 7407; DB 1; Length 1477;

Query Match

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; MOLECULE TYPE:
US-08-530-198-4
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                                                                               61 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
                                                                                                                       181 ARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 240
                                                                                                                                                               241 ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 300
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                                                                                                             121 NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180
                                                                      61 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
           0; Gaps
                                         1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
            0; Indels
100.0%; Prec. ....
   Best Local Similarity 100.0
Matches 1477; Conservative
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                                                                                                                                                                                    1201 KSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEA 1260
                                                                                                                                                                                                                                                               GSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVAGSDIKATSGTLVINAKDAK 1320
1021 DSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTV 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEBH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Shoemaker and Mattare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible sysTEM: PC-DOS/MS-DOS PatentIn Release #1.0, Version #1.25
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CURRENT APPLICATION NUMBER: US/08/530,198
APPLICATION NUMBER: 13-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-530-198-4; Sequence 4, Application US/08530198; Patent No. 5869065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-DEC-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFANT: (703) 415-0813
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1477 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIY: Arlington
STATE: Virginia
COUNTRY: U c ZIP.
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OPERATING SYSTEM:
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                                                                               121 NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDALINTNGFTASTLDISNENIK 180
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                                1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT
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   Length 1477;
                   0; Indels
  DB 2;
100.0%; Score 7407;
100.0%; Pred. No. 0;
live 0; Mismatches
      Best Local Similarity 100.
Query Match
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                                                                      TFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKDITSLKT 1140
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5876733-Typeable Haemophllus
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
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16-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/469,880
FILING DATE: 06-JUN-1995
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REGISTRATION NUMBER: 22,651
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FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PC
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker
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PRIOR APPLICATION DATA:
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STATE: Virginia
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22202-0286
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                                                                                                                        Query Match
100.0%; Score 7407;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1477; Conservative 0; Mismatches
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 4:
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1477 amino acids
                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                       TOPOLOGY: linear
                                                                                                     US-08-469-880-4
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              901 LTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVTNDGDLNITTHAKRNQR 960
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TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5928651-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoematon:
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
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PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-MAR-1993
FILING DATE: 10-MAR-1993
APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/0:
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ZIP: 22202-0286
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STATE:
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                                                                                                                                                                                                          DB 2; Length 1477;
                                                                                                                                                                                                        / Match 100.0%; Score 7407; Local Similarity 100.0%; Pred. No. 0;
                                                                                                                                                                                                                             0; Mismatches
                                                NAME: Berkstresser, Jorry W
REGISTRATION NUMBER: 22,651
REFENCE/COCKET NUMBER: 1038-633
TELEPHONE: (703) 415-0810
TELEPHONE: (703) 415-0813
TELEPHONE: CANADATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1477 amino acids
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                          Matches 1477; Conservative
                                                                                                                                                            STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                    amino acid
                                                                                                                                                                                US-08-728-470-4
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                                    781 NSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGG 840
                                                                                                           841 QNSSSSITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLVNGSLSLTGENADIKGN 900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 5977336-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1441 EFTTRPSSQVIISEGKACFSSGNGARVCTNVADDGQP 1477
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Patent No. 5977336
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-617-697-4
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                                                                                                                  APPLICATION NUMBER: US PCT/US93/02166 FILING DATE: 16-MAR-1993 ATTORNEY APAGENT INFORMATION:
                                                                                                                                                                        NAME: Berketresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 1038-557
TELECHMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR ESQ ID NO: 4:
SCHOLENCE CHARACTER 15TICS:
LENGTH: 1477 amino acids
           APPLICATION NUMBER: US/08/617,697
FILING DATE: 01-ARR-1996
CLASSIECATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-007-1994
                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 100.0
Matches 1477; Conservative
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single;
TOPOLOGY: linear
US-08-617-697-4
                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             amino acid
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1081 TENNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKDITSLKT 1140
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                                                                                                    841 QNSSSSITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLVNGSLSLTGENADIKGN 900
                                                                                                                                                                     901 LTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVTNDGDLNITTHAKRNOR 960
721 KLKPNENMNTSKPLPIRFLANITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTL 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Barenkamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: of No. 6218141-Typeable Haemophilus
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08719641 Patent No. 6218141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 7407; DB 4; Length 1477; 100.0%; Pred. No. 0; Live 0; Mismatches 0; Indels 0;
                                     COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,641
                                                                                                                                                                                                     US PCT/US93/02166
                                                                                                                                                    APPLICATION NUMBER: US 08/302,832
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    1038-625
                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
                                                                                                                                                                                                                                                                                      NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
                              Floppy disk
                                                                                                                                                                                                                 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1477 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 100.
Matches 1477; Conservative
             COMPUTER READABLE FORM:
                                                                                                                         CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                  APPLICATION NUMBER:
FILING DATE: 16-MAR
                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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22202-0286
                           MEDIUM TYPE:
                                                                                                                FILING DATE:
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Sequence 71, Application US/09206942 Patent No. 6432669 GENERAL INFORMATION: APPLICANT: Loosmore, Sheena M. APPLICANT: Yang, Yan-Ping

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APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High
TITLE OF INVENTION: Molecular Weight Proteins
FILE REFERENCE: 1038-861 MIS.;b
CURRENT APPLICATION UNMER: US/09/206,942
CURRENT FILING DATE: 1998-12-08
EARLIER APPLICATION UNMER: 09/167,568
EARLIER FILING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver. 2.1
EBNGTH: 1477
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                                                                                                                                                      DSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTV 1080
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                                                    LTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVTNDGDLNITTHAKRNQR 960
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STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 01-APR-1996
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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SOFTWARE: PatentT
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ZIP: 22202-0286
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CITY: A
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                                                                                                                                                                                                                                                                                                                   Query Match 71.3%; Score 5282; DB 2; Best Local Similarity 68.3%; Pred. No. 1.1e-292; Matches 1099; Conservative 136; Mismatches 231;
                        APPLICATION NUMBER: US 08/302,832
FILING DATE: 05-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                  1038-557
                                                                                                                   NAME: Berkstresser, Jerry M
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                     TELEPANNE: (703) 415-0810
TELEPAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1600 amino acids
          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                               amino acid
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CLASSIFICATION:
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                                                                                                                 NAME:
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955 AKRNQRSIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKEGNLTISSDKINITKQITIK 1014
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1131 VTSHKTINISAAAGNVTTKEGTTINATTGSVEVTAQNGTIKGNITSQNVTVTATENLVTT 1190
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                                                                                                                                                                                                                                                                                                                                                                    1075 AEAKTVTFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKD 1134
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|1311 GKLTSTVGSTINGTNSVTTSSQSGDIEGTISGNTVNVTASTGDLTIGNSAKVEAKNGAAT 1370
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717 KVNFKLKPNENMNTSKPLPIRFLANITATGG--GSVFFDIYANHSGRGAELKMSEINISN 774
                APPLICANT: LOOSMOTE, Sheena M. APPLICANT: LOOSMOTE, Sheena M. APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Michel H. TITLE OF INVENTION: Protective Recombinant Haemophilus Influenzae High TITLE OF INVENTION: Molecular Weight Proteins FILE REFERENCE: 1038-861 MIS:jb
                                                                              835 NVTLGGQNSSSSITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLVNGSLSLTGEN
                                                                                                                                                     836 NVTLGGENSSSSITGNINITNKANVTLQADTSNSNTGLKKRTLTLGNISVEGNLSLTGAN
                                                                                                                                                                                    ADIKGNLTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVTNDGDLNITTH
                                                            775 GANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGG
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us-10-092-880-4.rai

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US-08-038-682-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     923 FTNNGTAEINITQGVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSLNITDSNND 982
                                                                                                                                                                                                                                                                                                                             62 SRKLTVNSSINIGSNSHLILHSKGQRGGVQIDGDITSKGGNLTIYSGGWDVHKNITLD 121
                                                                                                                                                                                                                                                                                                                                                                        563 QGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTGKGLNII 622
                                                                                                                                                                                                                                                                                                                                                                                        623 SSVNNLTHNLSGTINISGNITINQTTRKNTSYWQTSHDSHWNVSALNLETGANFTFIKYI 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                        683 SSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFLANI 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 SSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFLANI 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           803 SNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGGQNSSSSITGNITIEKAANVTLE 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    863 ANNAPNOONIRDRVIKLGSLLVNGSLSLTGENADIKGNLTISESATFKGKTRDTLNITGN 922
                                                                                                                                                                                                                                                443 DNVSINAEDPLFNNTGINDEFPTGTGEASDPKKNSELKTTLTNTTISNYLKNAWTMNITA 502
                                                                                                                                                                                                                                                                                                             503 SRKLTVNSSINIGSNSHLILHSKGQRGGGVQIDGDITSKGGNLTIYSGGWVDVHKNITLD 562
                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                   Ouery Match 69.7%; Score 5164; DB 4; Length 1036; Best Local Similarity 99.5%; Pred. No. 3.4e-286; Matches 1030; Conservative 2; Mismatches 3; Indels 0;
CURRENT APPLICATION NUMBER: US/09/206,942 CURRENT FILING DATE: 1998-12-08 EARLIER APPLICATION NUMBER: 09/167,568 EARLIER FILING DATE: 1998-10-07 NUMBER OF SEQ ID NOS: 95 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                          GGANISM: Haemophilus influenzae US-09-206-942-73
                                                                                                               1036
                                                                                                SEQ ID NO 73
                                                                                                               LENGTH:
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                                                         1343 VTAATSSSVNITGDLNTVNGLNIISKDGRNTVRLRGKEIEVKYIQPGVASVEEVIEAKRV 1402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNKIYRLKFSKRLMALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEPH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURPACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
CORRESPONDENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Shoemaker and Mattare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: v.r.y...
COUNTRY: U.S.A.
ZIP: 2202-0286
ZIP: 2202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/038,682
...TARG DATE: 16-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08038682
Patent No. 5549897
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: BERKSTRESSER, JERRY W
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1536 amino acids
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                                                                                                                                                                                                                                                               1022 NGARVCTNVADDGQP 1036
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Q	121	I NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180	
à	181	RNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 24	
ΩD	181	ARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGGKIT	
ογ	241	ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQCKLSADSVSKDKSGNIV 30	
Op	241	ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQCKLSADSVSKDKSGNIV	
oy op	301	. LSAKEGEAEIGGVISAQNOQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGE 360 	
δy	361	GKNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWGDIALIDGNINAQGSGDIAKTGGFVET 42	
QQ	361	GRNGIQLAKKTSLEKGSTINVSGKEKGGRAIVWGDIALIDGNINAQGSGDIAKTGGFVET 42	
S S	421	SGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDEFPTGTG-EASDPKKNSEL 47.	
δ	1 00	KITLINITISNYLKNAMTMINITASRKITOVISCHULITTISKOONSASTPKRIKE- 47	
QQ	479	:    :      :	
ογ	540	LD-QGFLNITA-ASVAFEGGNNKARDAANAKIVAQ 59	
Op	538		
Qy	594	SSVNNLTHNLSGTINISGNITINQTTRK 65	
g	591	IT-SGNQKGFRFNNVSLNGTGSGLQFTTKRINKYAITNKFEGTLNISGKV	
Oy Db	651	NTS-YWQTSHDSHWNYSALNLETGANFTF-IKYISSNSKGLTTQYRSSAGVNFNGVNGNM 708       : ::  ::	
δλ	0	FNLKEGAKVNFKLKPNENMNTSKPLP-IRFLANITATGGGSVFFDIYANHSGRGAE 76	
Op	0	VERNARVNFDIKAPIGINKYSSLNYASFNGNISVSGGGSVDFTLLASSSNVQTPGVV 76	
Oy Dp	765	LKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAIN 824	
ογ	825	VNISILGGNVTLGGONSSSSITGNITIEKAANVILEANNAPNOONIRDRVIKLGSLIV AA	
Dp	825		
οy	885	SLSLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVT 94	
Dp	883		
δ	945	SILGEDIINKKGSLNITDSNNDAEIQIGGNISQKEGNLTISSDK 10	
QΩ	943	KNLSITTNSSSTYR	
δλ	1005	SISGENKAEITAKDG	
QQ	1003	NITKQITIKAGVDGENSDSDATNNANLTIKTKELKLTQDLNISGENKAEITAKD	
ογ	1065	GNSNDGNSGAEAKTVTFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLT	
qq	1063		
٥y	S	ISLKTVNITA-SEKVTTTAGSTINATNGKASITTKT-	
qq	22	NVTVNNNITSHKAVSISATSGEITTKTGTTINATTGNVEITAQTG	
ογ	171	SUL LISCIT 118	
QQ	1182 \	24	

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1182 VSVSATVDLTTKSGSKIEAKSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEIN 1241
                      1242 VEVKATESLTTQSNSKIKATTGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEIN 1301
                                                                                                        1242 ATEGAATLTATGNTLTTEAGSSITSTKGQVDLLAQNGSIAGSINAANVTLNTGTLTTVA 1301
                                                                                                                                                                                                                                                                         1302 GSDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVN 1361
                                                                                                                                                                                          1362 GLNIISKDGRNTVRLRGKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLG 1421
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Patent No. 560938

GENERAL INFORMATION:
APPLICANT: Barentamp, Stephen J
TITLE OF INVENTION: High Molecular Weight Surface Proteins
TITLE OF INVENTION: Of No. 5603938-Typeable Haemophilus
NUMBER OF SEQUENCES: 8
CORRESPONDENCES: 8
CORRESPONDENCES: 8
ADDRESSE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
67.1%; Score 4967; DB 1; Length 1536;
Best Local Similarity 67.3%; Pred. No. 9.3e-275;
Matches 1047; Conservative 146; Mismatches 264; Indels 98,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARES PATENTIAN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,832
FILING DATE: 16-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US pct/us93/02166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US pct/us93/02166 FILING DATE: 16-MAR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1038-404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Berkstresser, Jerry W
REGISTRATION NUMBER: 22,651
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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STATE: Virginia
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US-08-302-832-2
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Qy Dp	61	SIPQSVLASGLQGMDVVHGTATWQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN   	120
λō	0 0	SAVENRVISNOISQLKGILDSNCQVFLINPNGITIGKDALINTNGFTASTLDISNENIK 	180
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ος Op	301	SAKEGEAEIGGVISAQNQQAKGGKLMITGDKV 	360
QY	9 9	KNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWGDIALID 	0 0
Oy Dp		GHDLFIKDNAIVDAKEW 	479
Qy Db	9 7	KTTLFNTTISNYLKNAWTWNITASRKLTVNSSIN           KTTLFNTTLESILKKGTFVNITANORIYVNSSIN	m m
Qy Db	4 W	SKGGNLTIYSGGWUDVHKNITLD-QGFLNITA-F ::                   TGDDTRGANLTIYSGGWUDVHKNISLGAQGNINITAK	
Qy	594	GTVTITGEKDFRANNVSLNGTGKGLNIISSVNNLTHNLSGTINISGNITI   : :	650 649
ογ Ob	5 5	NTS-YWQTSHDSHWNVSALNLETGANFTF-I 	708
Oy Db	0 0	SFULKEGAKVNFKLKPNENMNTSKPLP-IRFLANITATGGGSVFFDIYANHSG-    :  :  :  :  :  :  :  :  :  :  :     FFNVERNARVNFDIKAPIGINKYSSLNYASFNGNISVSGGGSVDFTLLASSSNV	764
Oy Dp		LKMSEINISNGANFTLNSHVRGDDAFKINKDLFINATNSNFSLROT :	824
QY	0, 0,	STYNISILGGNVTLGGQNSSSSITGNITIEKAANVTLEANNAFNQON :   :   :      :	884
Oy Db		NGSLSLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGTAEINI	944
Oy Db	4 4	DGDLNITTHAK : :  :: SKNLSITTNSS	1004
oy da	1005	INITKOITIKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLT 	1064

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1362 GLNIISKDGRNTVRLRGKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKIG 1421
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                                                                                                                                                                                                                                                                                                                         1242 ATEGAATLTATGNTLTTEAGSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVA 1301
               1063 IGNTNSAD-GTNAKKVTFNQVKDSKISADGHKVTLHSKVETSGSNNNTEDSSDNNAGLTI 1121
                                                            1125 TAKNVEVNKDITSLKTVNITA-SEKVTTTAGSTINATNGKASITTKT------ 1170
                                                                                                                      -----GDISGTISGNT 1181
                                                                                                                                                    1182 VTLTATEGALAVSNISGNTVTVTANSGALTTLAGSTIKGTESVTTSSQSGDIGGTISGGT 1241
1065 IGNSNDGNSGAEAKTVTFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTI 1124
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BARENKAMP, STEPHEN J
APPLICANT: ST. GEME III, JOSEBH W
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT SURFACE PROTEINS
TITLE OF INVENTION: OF NON-TYPEABLE HAEMOPHILUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: Shoemaker and Mattare, Ltd
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CVERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPLICATION NUMBER: US/08/530.198
FILING NAME.
                                                                                                                            1171 ------
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13-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 2, Application US/08530198; Patent No. 5869065; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22202-0286
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202-0286
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STRANDEDNESS: Sir
TOPOLOGY: linear
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                                                                                       1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
                                                                                                       480 KTTLTNTTISNYLKNAWTMNITASRKLTVNSSINIGSNSHLILHSKGQRGGGVQIDGDIT 539
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                                     Query Match 67.1%; Score 4967; DB 2; Length 1536; Best Local Similarity 67.3%; Pred. No. 9.3e-275; Matches 1047; Conservative 146; Mismatches 264; Indels 98
    protein
MOLECULE TYPE:
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US-08-530-198-2
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                                                   1065 IGNSNDGNSGAEAKTVTFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTI 1124
                                                                                                                  1125 TAKNVEVNKDITSLKTVNITA-SEKVTTTAGSTINATNGKASITTKT------- 1170
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                                1005 INITKOITIKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: of No. 5876733-Typeable Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza;
STREET: Bldg. 1
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,880
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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APPLICATION NUMBER: GB 9205704.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barenkamp, Stephen J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08469880 Patent No. 5876733 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16 WAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PC
FILING DATE: 16-MAR-1993
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CORRESPONDENCE ADDRESS:
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STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 ARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 SIPOSVLASGLOGMDVVHGTATMQVDGNKTIIRNSVDAIINWKOFNIDQNEMVQFLQENN 120
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                                                                          1038-516 MIS:vg
                                NAME: Berkstresser, Jerry W Redistration UMBER: 22,651
REPERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEFONE: (703) 415-0810
TELEFAX: (703) 415-0810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1536 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (genomic) US-08-469-880-2
FILING DATE: 16-SEP-1994 ATTORNEY/AGENT INFORMATION:
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                                                                               825 AKKNITFEGGNITFGSRKAVTEIEGNVTINNNANVTLIGSDFDNHQ--KPLTIKKDVIIN 882
                                                                                                                                                     883 SGNLTAGGNIVNIAGNLTVESNANFKAITNFTFNVGGLFDNKGNSNISIAKGGARFKDID 942
                  885 NGSLSLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVT 944
765 LKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAIN 824
                                                          825 STYNISILGGNVTLGGQNSSSSITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLV 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: High Molecular Weight Surface Proteins TITLE OF INVENTION: Of NO. 5928651-Typeable Haemophilus NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS: ADDRESSE: Shoemalor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: 2001 Jefferson Davis Hwy., 1203 Crystal Plaza
STREET: Bldg. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08728470 Patent No. 5928651
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MEDIUM TYPE: Floppy
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ZIP: 22202-0286
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                           FILING DATE: 16-MAR-1993
FILING DATE: 16-MAR-1993
APPLICATION NUMBER: US PCT/US93/02166
FILING DATE: 16-MAR-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/728,470
                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,832
                                                                                                                                                                                                                                                        1038-633
                                                                                                                                                                            APPLICATION NUMBER: GB 9205704.1
FILING DATE: 16-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Berkstresser, Jerry
REGISTRATION NUMBER: 22,651
                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                        1536 amino acids
                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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Best Local Similarity
                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE:
US-08-728-470-2
                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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538 TGDDTRGANLTIYSGGWVDVHKNISLGAQGNINITAKQDIAFEKGSNQV-----ITGQ 590
                        594 GTVTITGEGKDFRANNVSLNGTGKGLNIISSVNN---LTHNLSGTINISGNITINQTTRK 650
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                                        651 NTS-YWQTSHDSHWNVSALNLETGANFTF-IKYISSNSKGLTTQYRSSAGVNFNGVNGNM 708
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                                                                                                                          709 SFNLKEGAKVNFKLKPNENMNTSKPLP-IRFLANITATGGGSVFFDIYANHSG---RGAE 764
                                                                                                                                          1182 VTLTATEGALAVSNISGNTVTVTANSGALTTLAGSTIKGTESVTTSSQSGDIGGTISGGT 1241
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Search completed: March 24, 2003, 15:24:58 Job time : 28 secs

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March 24, 2003, 15:21:24 ; Search time 18 Seconds
    (without alignments)
    3403.363 Million cell updates/sec
                                                                                                                                                                                                                    Title: US-10-092-880-4
Perfect score: 7407
Sequence: 1 MNKIYRLKFSKRLNALVAVS.......CFSSGNGARVCINVADDGQP 1477
                                                                                                                                                                                                                                                                                                                                                                                                                                112892
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                   112892 segs, 41476328 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database :
                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	991				P45354 haemophilus					es		Sa		Se	Q53020 r outer mem	P96989 r outer mem				escherich	-		Q9pjy2 chlamydia m	-	_		<u> </u>		P35828 caulobacter	-	٦	~	P15292 lactococcus
SUMMARIES		HLYA_PROMI	YDBA_ECOLI	OMPA_RICRI	HXA3_HAEIN	HXA2_HAEIN	OMPB_RICJA	OMPA_RICCN	FHAB_BORPE	HXA1_HAEIN	YDEK_ECOLI	OMPB_RICRI	BIGA_SALTY	OMPB_RICCN	HLYA_SERMA	OMPB_RICPR	OMPB_RICTY	YEEJ_ECO57	AIDA_ECOLI	YEEJ_ECOLI	YPJA_ECOLI	PMPB_CHLTR	IGAO_HAEIN	PMPB_CHLMU	CBPA_CLOCL	IGA2_HAEIN	PM20_CHLPN	PMPC_CHLTR	120K_RICRI	SLAP_CAUCR	YFAL ECOLI	P2P_LACPA	P2P_LACLC	P3P_LACLC
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1341 1310 1253 1902 1902 1947 1541 1849 11861 11863 1176	PROMI STANDARD; PRT; 157  36. 1990 (Rel. 15, Last sequence upd  70-1990 (Rel. 16, Last sequence upd  70-1990 (Rel. 16, Last sequence upd  1ysin precursor.  Enia; Proteobacteria; gamma subdivi  enia; Proteobacteria; gamma subdivi  ens.  FINE-90109827; PubMed-2407716;  ff T.S., Welch R.A.;  1ectide sequencing of the Proteus m  14a marcescens hemolysin genes (sh  172:1266-126(1990).  FUNCTION: BACTERIAL HEMOLYSINS ARE  CUELL MEMBRANES AND CAUSE CELL RUPTU  FUNCTION: BACTERIAL HEMOLYSINS ARE  FUNCTION: CELL-BOUND HEMOLYSINS ARE  FUNCTION: CELL-BOUND HEMOLYSINS ARE  FUNCTION: CELL-BOUND HEMOLYSINS ARE  FUNCTION: STAND CAUSE CELL RUPTU  SUBCELLULAR LOCATION: OUSE CELL RUPTU  SUBCELLULAR LOCATION: OUSE PROMITE  AND TON-POSITE FOR PORE FORMATI  SMISS-PRY ENTY; TO S.MARCESCENS HEMOLY  SMISS-PRY ENTY IS COPYIGHT. IT  SMISS-PRY ENTY IS COPYIGHT. IN  SMISS-PRY ENTY IS COPYIGHT. IT  SMISS-PRY ENTY IS COPYIGHT. IN  A MACH  A MACH  A MACH  A MACH  B MACH  A MACH  A MACH  A MACH  B MACH  A MACH  A MACH  B MACH  A MACH  A MACH  B MACH  A MACH  A MACH  A MACH  B MACH  A MACH  B MACH  A MACH  A MACH  B MACH  A MACH  B MACH  A MACH  A MACH  B MACH  A MACH  A MACH  B MACH  A MACH  B MACH  A MACH  B MACH  A MACH  B MACH  A MACH  A MACH  B MACH  A MACH  B MACH  A MACH  A MACH  B MACH  A MACH  A MACH  B MACH  B MACH  A MACH  B M	SGRLAASL
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g	115	SRNPSFLLGQQEVFGIAAEYVLSNPNGITCDGCGF	
oy d	187	EQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGGKITI 24	
ð	242	SDIINPITTYS	
qq	222	SQHFDILSSQKPVSALDS	
δý	282	NQGKLSADSVSKDKSGNIVLSAKEGEAEIGGVISAQNQQAKGGK	
Dp	282	TDSQVRYDSYDKDGSENYQNYRGGITVNNSGSSQTLTKTELKGKNITLVASSHNQIKASD 34	
٧٥ ۾	326	LMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGEGKNGIQLAKKTSLEKGSTINV	
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Οy	416	GFVETSGHDLFIKDNAIVDAKEWLLDFDNVSI 44	
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ò t	557	KNITLDQGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTIGEG	
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67 07 08	647	TTRKNTSYMQTSHDSHWNVSALNLETGANFTFIKYISSNS 686	
ò	687	PSSAGVNE-NGVNCNMSDNI FFGSDLATI TAGNASI TGDNVAFVSTEN	
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q	816	DLITTANKDLLHEGASHHVEGRYQESGENIQHLAVNDSETSKTDSLNVGIDVGVN 870	
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qq	871	LDYSGVT-KPVKKALEDGVNTTKPGNNTDLTKKVTARDALANLANLSNLETPNVGVEVGI 929	
χχ	839	GGQNSSSSITGNITIEKAANVTLEANNAPNQQNIRDRVIKLG-SLLVN 885	
g G	930	KGGGSQQSQTDSQAVSTSINAGKIDIDSNNKLHDQGTHYQSTQEGISLTANTHTSEATLD 989	
λ	886	GSLSLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGT 928	
g G	0	KHQTTFHETKGGGQIGVSTKTGSDITVALKGEGQTTDNALMETKAKGSQFTSNGD 1044	
λ	929	AEINITQGVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSLNI:TDSNNDAEI 985	

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986 QIGGNISQKEGNLTISSD------KINITKQITIKKGIDGEDSSSDATSNANLTIKT 1036
                                                                     1037 KELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEA---KTVTFNNVKDSKISAD 1093
                                                                                                                                   1094 GHNVTLNS------KVKTSSSNGGRESNSDNDT--GLTITAKNVEVNKDITSL---- 1138
                                                                                                                                                                                                    1203 G----LGSAQFAIGKQDEKSVSREGGTINNSGNLTINGNSVHLQGAQVNSKDTQLTSQSG 1258
                                                                                                                                                                                                                                             1139 ----KTVNITASEKVTTTAGSTINATNGKASITT----KT 1170
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                                                                                                                                                                                                                                                                           1259 DIEITSAOSTDYKNNWGTDIGFNGKKTNNTPKEVTEEKPATSIHNIGGKLLVNVEDOQKT 1318
                                                                                                                                                                                                                                                                                                                                 1369 HVTVGVNVGYNHTNDPKSSQVNKTAKAGGSLLEKTIKDTIDSGIKSSTDAISDKYNSLSS 1428
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Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
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SEDUENCE FROW N.A.
STRAIN-KIZ / MG1655,
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    398 VNNEGESAI----TNGGTGTQINGDDATANNNGKTTVDGKDSTGTEIAGNNGKVIQ--- 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 NAQGSGDIAKTGGFVETSGHDLFIK-DNAIVDAKEWLLDFD----NVSINAEDPLFNNTG 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      459 INDEFPTGTG---EASDPKKNSELKTTL----TNTTISNYLKNAWTMNITASRKLTVNS 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KTI-IRNSVDAIINWKQFNIDQNE--MVQFLQENNNSAVFNR---VTSNQISQLKGILDS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 NGQVFLINPNG--ITIGKDAIINTNGFTASTLDISNENIKARNFTFEQTKDKALAEIVNH 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 GLITVGKDGS---VNLIGGKVKNEGVISVNGGSISL-LAGQKITISDIINPTITYSIAAP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       236 ----GKDSTGTEINGNNGKVIQDGDLDVSGGGHGIDITGDSATVDNKGTMTVT----DP 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 ESMGIQIDGDKALVNNEGESTITNGGTGTQINGDDATANNNGKTTVDGKDSTGTEINGNN 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 GKVIQDGDLDVSG------GGHGIDITGDSATVDNKGTMTVTDPESIGIQVDGDQAV 397
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Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishlo Y., Oshima T., Saito N., Sampel G., Seli Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., "A 570-kb Dha sequence of the Escherichia coli K.12 genome Corresponding to the 28 0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 21.7%; Pred. No. 3.6e-14;
Matches 388; Conservative 229; Mismatches 625; Indels 542; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 KTLTIRDSV-----FTYTENADGTISLQDSNGRKATINLWQIDEANNTVALEGVSAD 204
                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG (AC P25928).
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR THIS PROPEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT BETWEEN AMINO ACIDS 839 AND 840.
                                                                                                                                                                                                                                                     Moszer I., Glaser P., Danchin A.; "Multiple IS insertion sequences near the replication terminus in Escherichia coli K-12." Biochimie 73:1361-1374(1991).
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2003 AA; 205949 MW; B83A12C8B53220EE CRC64;
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EMBL; AE000237; AAC74487.1; ALT_SEQ.
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D90778; BAA18880.1; ALT_SEQ
D90779; BAA18881.1; ALT_SEQ
X62680; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                              MEDLINE-92190338; PubMed-1665988;
                                                                                                                                                                                     SEQUENCE OF 464-2003 FROM N.A.
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Hypothetical protein;
CONFLICT 489 48
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                                                                                                                                  511 SI----NIGSNSHLILHSKG-----QRGG-GVQIDGDITSKGGNLTIYSGGWVDVHK--- 557
                                                                                                                                                                                                                  556 GAHGVENIGDNG--TVNNKGDIVVSDTGSIGVLINGE-----GATVSNTGDVNVSNEAT 607
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                                                      SIAGSINAANVTLN-----TTGTLTT-----VAGS---DIKATSGTLVINAKDAK 1320
1524 NVEGMNGN--NGNSSEVHYGDYTLPDVPKPNTVSVTSGSDEAGGSMNNLNGYVVGTNVNG 1581
                                                                                                          1582 S-AGKLKVNNASMNGVEINTGFTAGTADTTVSFDNVVEGSNLTDADAITSTSVV--WTAK 1638
                                                                                                                                                                       1321 LNGDASGDSTEVNAVNASGSGSVTAATSSSVNITG---DLNTVNGLNIISKDGRNTVRLR 1377
                                                                                                                                                                                                              1378 GKEIEVKYIOPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLGVSAVRFVEPNNTITVN 1437
                                                                                                                                                                                                                                                                                                                                              1695 SALKQVS----GSQATTVFREARVLSNRFSMLADAAPKVGNGLAFNVVAKGDPRAELGNN 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71-324.
71-3787-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last Sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Outer membrane protein A precursor (190 kDa antigen) (Cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;

"A protective protein antigen of Rickettsia rickettsii has tandemly repeated, near-identical sequences.";

Infect. Immun. 58.2760-2769(1990).

-: FUNCTION: ELICITS PROTECTIVE IMMUNITY.

-: SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A STAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 X APPROXIMATE TANDEM REPEATS.
A (TYPE I).
C (TYPE II).
C (TYPE II).
E (TYPE II).
E (TYPE II).
F (TYPE I).
I (TYPE I).
I (TYPE I).
J (TYPE I).
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-1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision, Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
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Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                        1438 TQNEFTT-----RPSSQVIISEGKACFSSGNGARVCTNVADDG 1475
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1751 TEYDMLALRKTIDLSESQTMSLEYGIARLDGDGAQ----KAGDNG 1791
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InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 OSAAPSKITLA---GNIDGGGIITVKTDAAINGTIGNTNALATVNVGA------GTA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 TLGGAVIKATTIKLINAASVLTLINANAVLTGAIDNTTGGDNVGVLNLNGALSQVTGDIG 288
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                                                                                                                                    Best Local Similarity 22.1%; Pred. No. 1.1e-13;
Matches 335; Conservative 197; Mismatches 593; Indels 388; Gaps
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950 1021 K (TYPE II).
1022 1093 L (TYPE II).
104 1165 M (TYPE II).
1166 1180 TYPE I (INCOMPLETE).
2249 AA: 224333 MW; A9D6646C089DF087 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1433 TITV-----ISEGKACFS 1460
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1014 KKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDG-- 1071
                                                                        -----SKVKTSSSNGGRE 1113
                                                                                                                                           1114 SNSDNDTG-----LT1TAKNVEVNKDI---TSLKTVNITASEKVTTTAGSTINATNGKA 1164
                                                                                                         863 NLNGALSQVTGDIGNTNSLATISVGAGTATLGGAVIKATTTKLTNAASVLTLTNANAVLT 922
                                                                                                                                                                               923 GAIDNTTGGDNVGVLNLNGALSQVTGDIGNTNSLATISVGAG--TATLGGAVIKAT---- 976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Heme/hemopexin-binding protein precursor (Heme:hemopexin utilization
                                    810 SVG-----AGTATLGGAVIKATTTKLTNAASVLTLTNANAVLTGAVDNTTGGDNVGVL 862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mueller-Eberhard U., Hansen E.J.;
"The 100 kDa haem:haemopexin binding protein of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-9511556; PubMed-7815944;
MEDLINE-9511556; PubMed-7815944;
MEDLINE-9511556; PubMed-7815944;
Mueller-Eberhard U., Hansen E.J.;
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Mol. Microbiol. 13:863-873(1994).
                                                                            1072 --NSGAEAKTVTFNNVKD-SKISADGHNVTLN----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 IDLSGKEGGETYLGGDERGEGKNGIQLAKKTSLEKGS-TINVSGKEKGGFAIVWGDIALI 399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | : | : : : : : : | | | : | 363 NIDVPGAENIRIADDKDNTETDSFIOTEALSSLLANNGKVNLKGN-DVNISGNINIDSFR 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       478 MGLGRSVNEDDYATRWK-----RAEKSQRKKFNVDMRNV-----VFNQVDEVI--L 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           233 LLAGQKITISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293 KDKSGNIVLSAKEGEAEI-----GGVISAQNQQAKGGKLMITGDKVTLKT----GAV 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 NENIKARNFTFEQTKDKAL---AEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSIS 232
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
6.9%; Score 509; DB 1; Length 917;
Best Local Similarity 24.4%; Pred. No. 4.4e-14;
Matches 254; Conservative 167; Mismatches 372; Indels 248; Gaps
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                                                                                              BY SIMILARITY.
HEME/HEMOPEXIN-BINDING PROTEIN
3 X 5 AA TANDEM REPEATS.
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917 AA;
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                                                                                                                                                                                                                                                                                                      951 ITTHAKRNQRSIIGGDI-INKKGSLNITDSNNDAELQIGGNISQKEGNLTISSDKINITK 1009
-----LDLDYRTQLS----- ELEQGRR-RWRYRDLDLDMNKAYLYR---- 594
                                                         642 DITFDKDNSQDTLAQTNRLGMNGKV-SMINS--HIKIVGDEKEGISPTGTYATWFLIGEL 698
                                                                                                                                                                                                                                                             742 ITATGGSVFFDIYA-NHSGR----GAELKM--SEINISNGANFTLNSHVRGDDAFKINK 794
                                                                                                795 DLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGG----NVTLGGQNSSSSITGNI 851
                                                                                                                                                                     852 TIEKAA-----SLLVNGSLSLT 891
                                                                                                                                                                                                     699 IGEKSSIFVKSHQGYTFKTDGDTKIAGKN--SKEDLKITAINTGGRAAEEVLINGALGSA 756
                                                                                                                                                                                                                                     892 GENADIKG-NLTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVTNDGDLN 950
                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Heme/hemopexin-binding protein precursor (Heme:hemopexin utilization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cope L.D., Yogev R., Mueller-Eberhard U., Hansen E.J.; "A gene cluster involved in the utilization of both free heme and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=D142 / Serotype B. STRAIN=D142 / Serotype B. STRAIN=D142 / Serotype B. STRAIN=D118556; PubMed-7815944; Cope L.D., Thomas S.E., Latinar J.L., Slaughter C.A., Mueller-Eberhard U., Hansen E.J.; The 100 Kba haemishaemopexin-binding protein of Haemophilus influenzae: structure and localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEME/HEMOPEXIN-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heme hemopexin by Haemophilus influenzae type b.";
J. Bacteriol. 177:2644-2653(1995).
-!- FUNCTION: BINDS HEME/HEMOPEXIN COMPLEXES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    928 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 22-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=DL42 / Serotype B;
MEDLINE=95270579; PubMed=7751272;
                                                                                                                                                                                                                                                                                                                                                                        1010 QITIKKGIDGEDSSSDATSNA 1030
                                                                                                                                                                                                                                                                                                                                                                                                         873 LVS---SLDVEKLVSVAVCDA 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U08348; AAA74138.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haemophilus influenzae.
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NCBI_TaxID=727;
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P45354;
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Gaps
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                                                                                                                                                                                                                                                                                                                                                  193 ALAEIVNHGLITVGKDGSVNLIGGKVKNEGVIS------VNGGSISLLAGQKIT 240
                                                                                                                                                                                                                                                                                                                                                                                                                   152 ---QVLKEGLVL--KDGQY-VKEGQVINEGNITAQDFVVLNGDEVINKGNINVEKNSTIN 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 ISDIINPTITYSIAAPENE-AVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 GKVYLSSGYNFTFTLPDSGISVALED-----NTVQGIVKNEGSI------KAGEI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 VLSAKEGEAEI-----GGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYL 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 GGD--ERGEGKNGIQLAKKTSLEKGS-TINVSGKEKGGFAIVWGDIALIDGNINAQGSGD 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 GADVISNKELKDNIKIISKTGSKVTSPKINFICKSVN------INGNFGREDS-- 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 IAKTGGFVETSGHDLFIKDNAIVDAKEWLLDF-DNVSINAEDPLFNNTGINDEFPTGTGE 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    470 ASDPKKNSELKTTLINTISNYLKNAWTMNITASRKLTVNSSINI----GSNSHLILHSK 525
                                                                                                                                                                                                                                                                                         352 -----TTHYKDEFKKLNTEVN----IDVPDNENIRIAD-IEDNTGTG---TTGTGT 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        395 SS------FIQTCALSSLLANNGKVNLKGN-NVNISGRIHIDSFRGSDSLLKLTNK 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             526 GQRGGGVQI-DGDITSKGGNLTIYS-GGWVDVHKNITLDQGFLNITAASVAFEGGNNKAR 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    444 GH---IDINNADIHSKGRLFFITSLONEEDFKSNITITDSKINLGNGAMGL-GRSVDEK 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         584 DAANAKIVAQGTVTITGEGKDFRANNVSLN-----GTGKGLNIISSVNNLTHNLSGT 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            499 DYDNRWQKTEGS---QRKKEDVKMSNVEFNQVDDVILAGGFEKVNLDKIV-----ATGQ 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   636 IN--ISGNITINQTTRKNTSYWQTSHDSHWNVSALN------LETGANFTFIKYI 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               550 TNFYIDGGVSRN---GRKYEYGVLDLDKRTQLSELNQGRRRWGYYYDLELDWNRAYL--- 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              683 SSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFLANI 742
                 1-1.
1-2.
1-3.
1-5.
1-6.
4 X 6 AA APPROXIMATE TANDEM REPEATS.
2-1.
2-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTL-GGQNSSSSITG---- 849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FDLFATKNTGRSTIKDTEINISN-SNINLKNGFVHLLAEKIKLDNSKI--D 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           554 ITEDKDNSQDTLAQT-----NRLGMNGKVSMINSHIKIVGDEKEGISPTGTYATM 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 TLSAKGRKQALDSLVMNNGVLEATKVSNKNGKVVLSADNVELNNESNI-----KGEIVTF
                                                                                                                                                                                                                                                    267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----YR------Y
                                                                                                                                                                                                                     DB 1; Length 928;
    X 6 AA APPROXIMATE REPEATS
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                      2-4.
7: 67D45466A4B92390 CRC64;
                                                                                                                                                                                                                                  llarity 23.8%; Pred. No. 3.7e-13;
Conservative 166; Mismatches 363;
                                                                                                                                                                                                                     Score 486.5;
                                                                                                                                                                                   101228 MW;
                                                                           640
679
172
154
160
166
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                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                          Matches 249;
                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
                                                                                                                                     947 GDLNITTHAKRNQRSIIGGDI-INKKGSLNITDSNNDAEIQIGGNISQKEGNLTISSDKI 1005
                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer membrane protein B precursor (168 Kba surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
(rOmp B) [Contains: 120 Kba surface-exposed protein (Surface protein antigen) (120 kba outer membrane protein ompB); 32 kba beta peptide].
850 ------NITIEKAANVTLEANNAP-----NQONIRDRVIKLG----SLLVNGS 887
                              704 FLIGELIGEKSSIFVKSHQGYTFKTDGNTKIAGKYSKEDLKITAINTGGRAAEEVLINGA 763
                                                                  888 LSLTGENADIKG-NLTISESATFKGKTRDTLNITGNFTNNGTAEINITQGVVKLGNVTND 946
                                                                                        -i - FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cchiyama T.: sequencing of the gene encoding the protein rOmp B of Rickettsia sequencing of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 KDA SURFACE-EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
POLY-GLY.
MW: 3132A69C9DD5999F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LAYER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rickettsia japonica.
Sacteria: Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsiaea; Rickettsia.
                                                                                                                                                                                                                                                                                                                                PRT; 1656 AA.
                                                                                                                                                                                                           1006 NITKQITIKKGIDGEDSSSDATSNA 1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB003681; BAA20138.1; -.
InterPro; IPR003858; rOmpA_rOmpB.
Pfam; PF02708; rOmpA_rOmpB; 1.
                                                                                                                                                                                                                                              880 INTKLVS---SLDVEKLVSVAVCDA 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         528 533 POI
1656 AA; 168097 MW;
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CHAIN 1 1338
CHAIN 1339 1656
                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                    OMPB_RICJA
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741 VF----NAGGK------ 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              819 GPINVTLNKQAVP-----VNALKQITVSG------PGNVVVNEIGNAGNYHG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            912 KTRDTL------INITGN-----FTNNGTAE-----INITQG 936
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        937 VVKLGNVTNDGDLNITTHAKRNQRSIIG------GDIINKK-----GSLNITDSNNDA 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          635 TILNGGNVAINELVIGNNGSVQFAHNTYLITRTINAAGQGKIIFNPVVNNNT-----T 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                695 SSAGVNF-NGVNGNMSFNL-KEGAKVNFKLKPNENMNTSKPLPIRFLANITATGG--GSV 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          751 FFDIYANHSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQT 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      811 KDDFYDGYARNAINSTYNISILGGNVTLGGQNSSSSITGNITIEKAA------- 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               776 ------LGNATFN----GNTTIAA-NSTLQISGNYTADFIASADGTGIVEFVNT 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    413 --DIMILIGNE---TGDANNPGNTAGVITFAANGTLASASADA---NVAVINNITALEAS 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   568 ITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNG------TGKGLN 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 GDIALIDGNINAQGSGDIAKTGGFV-ETSGHDLFIKDNAIVDAKEWLLDFDNVSINAEDP 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 -QSANANGOVNFRHIVDVGIDGTTAFKTAASIVAITQNSNFGT----TDFGNLAAQVTVP 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              453 LFNNTGINDEFPTGTGEASDPKKNSELKTTLTNTTISNYLKNAWTMNITASRKLTVNSSI 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513 NIG----SNSHLILHSKGQRGGGVQI-DGDITSKGGNLTIYSGGWVDVHKNITLDQGFLN 567
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Query Match
Best Local Similarity 21.8%; Pred. No. 1.9e-12;
Matches 346; Conservative 204; Mismatches 598; Indels 437; Gaps

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984 EIQIGGNISQKEGNL----TISSDKINITKQITIKKGID--GEDSSSDATSNANLTIKT 1036
                                                                                                                          964 IVTLSGGVPNTPGTVYGLGTGASKF---KQVTFTTDYNNLGNIATNTTINDGVTVTT 1020
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920 VIADGQVIGD------QNNIVGLGLGSDNGIIVNATTLYAGIGTIN----NNQG 963
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Crocquet-Valdes P.A., Weiss K., Walker D.H.;
"Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia
conorii (Malish 7 strain).";
Gene 140:115-119(1994).
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MEDLINE-97015921; PubMed-8862558;
Roux V., Fournier P.E., Raoult D.;
"Differentiation of spotted fever group rickettsiae by sequencing and
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
autigen) (rOmpa) (rOmp A).
OMPA OR RC1273.
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Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
Raoult D.,
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Q52657; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;
Q52670; Q52674;
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
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analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein rOmpA.", J. Clin. Microbiol. 34:2058-2065(1996).
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T -> II (IN STRAIN INDIAN TICK TYPHUS).

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M -> I (IN STRAIN INDIAN TICK TYPHUS).

O -> K (IN REF. 1).

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V -> I (IN REF. 1).

G -> D (IN REF. 1).

IS -> VN (IN REF. 1).

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VN -> IS (IN REF. 1).

VLRVQGGVKSNTIN -> KATLGGALIKATTTK (IN REF. 1).

D -> Y (IN REF. 1).
                                                                           STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;
Raoult D., Fournier P.E., Roux V.;
"Phylogenetic analysis of spotted fever group rickettsiae by study
                                                                                                                         Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein;
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Pfam; PF02708; rOmpA_rOmpB; 1.
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                                                             SEQUENCE OF 953-2012 FROM N.A.
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1304 FNAKNGTVTL-------NNNVAGTVKNTGGTNNGTLIVLGASNLNRVNGIAM 1350
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                                                                                                                                                                                                           952 TTHAKRNQRSII------GGDIINK--KGSLNITDSNND------- 982
813 QGCVVKSNTINLTDNASAVTFTNPVVVTG----AIDNTGNAN--NGIVTFTG---DSTVT 863
                                         849 GNITIEKA-ANVTLEANNAPNQQNIRDRVIKLGSLLVNGSLSLTGENA------ 895
                                                                                                                             896 ---DIKGNLTISESATFKGKTRDTLNITGNFTN-NGTAEINITQGVVKLGNVTNDGDLNI 951
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                                                                                                                                                                                                           Relman D.A., Domenighini M., Tuomanen E., Rappuoli R., Falkow S "Filamentous hemagglutinin of Bordetella pertussis: nucleotide sequence and crucial role in adherence.", Proc. Natl. Acad. Sci. U.S.A. 86:2637-2641(1989).
                                                                                         Relman D.A., Domenighini M., Tuomanen E., Rappuoli R., Falkow "Genetic characterization of Bordetella pertussis filamentous haemagglutinin: a protein processed from an unusually large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3591;
 Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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SEQUENCE 3591 AA; 367420 MW; EF7418B30D6E5138 CRC64;
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EMBL; M60351; AAA22976.1; ALT_INIT.
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                                                                                                                                                                                                 MEDLINE-89202384; PubMed-2539596;
                                                                           MEDLINE-90355839; PubMed-2388559;
                                                                                                                                                      Mol. Microbiol. 4:787-800(1990).
                                                                                                                                                                               SEQUENCE OF 1-3261 FROM N.A.
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01-NOV-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Heme/hemopexin-binding protein precursor (Heme:hemopexin utilization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 --IKINHADIHSTGRLFFITSLQNEKDSQSDITITDSKINLGNGAMGLGRSLDKENCDNQ 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    597 KDTEINISNSKINLKNGFVHLLAEKIKLDNSKIDITFDK---DNSQDISTQ-----INR 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        698 HQGY------ 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            874 DRVIKLGSLLVNGSLSLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGTAEINI 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         752 NMAFTIGD---NANTKTTIENAD--------ITALAPNGGTAYLS- 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    934 TQGV-VKLGNVTNDGDLNITTHAKRNQRSIIGGDI-INKKGSLNITDSNNDAEIQIGGNI 991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 KKNSELKTTLTNTTISNYLKNAWTMNITASRKLTVNSSINI----GSNSHLILHSKGQRG 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 -----SFIQTGALSSLLANNGKVNL-KGKDVNISGRIHIDSFRGSDSLLKLTNQGH-- 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   530 GGVQID-GDITSKGGNLTIYS-GGWVDVHKNITLDQGFLNITAASVAF------575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             576 ----EGGNNKARDAANAKIVAQ--GTVTITGEGKDFRANNVSLNGTGKGLNIIS---SV 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       480 RWCRIETSORKKEDVHMRNVVFDQVDDVVVAGGFKKVNLDNIV--ATGKTNFYIDGGVSR 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    626 NNLTHNLSGTINISGNITINQTTRK------NTSYW------QTS 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         538 NNSRYEY-GVLDLDKRTLLSELDQRRRRWKYYNDLDLDMNKAYWHRFDMFATKNTGRSTI 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            659 HDSHWNV--SALNLETG-------ANFTFIKYISSNSKGLTTQYRSSAGVNF 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                648 LGMNGKVSM-----VNSHIKIVGDEKSDISAKAPYATMFLIGELIGEKSSIF---VKS 697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           758 HSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDG 817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 ---TNEPKNKIKITSQTGSKVTSPKINFTGKSV-------NIN----GDFGR 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 TGGFVETSGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDEFPTGTGEASDP 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         329 D----DSKAH--YNEEHKRLDTE-----VNIDVPDNENIRIAEKDNIGIGIGTD- 371
                                                                                                                                 72 QCMDVVHGTATMQVDGNK-TIIRNSVDAIINWKQFNIDQNEMVQFLQENNNSAVFNRVTS 130
                                                                                                                                                                                                                                                      187 EQTKDKAL---AEIVNHGLITVGKDGSVNLIGGKVKNEGVI-SVNGGSISLLAGQK--IT 240
                                                                                                                                                                                                                                                                                                                                              241 ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 LSD----SSISVALEDNAVQSI-----VQNEGII------KAGDIT 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 LSAKEGEAEI-----GGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            236 LNAKGRNQALDSLVMNNGVLEATKVSNKNGKVVLSADDVQLNNKS--DIKGE--SEVVF- 290
                                       6.3%; Score 466; DB 1; Length 905;
llarity 23.7%; Pred. No. 2.5e-12;
Conservative 153; Mismatches 347; Indels 308; Gaps
                                                                                                                                                                                                                         131 NQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDI----SNENIKARNFTF 186
                                                                                                                                                               905 AA; 98833 MW; 2424013EB437A99D CRC64;
                                                                       Similarity
                                                                          3est_Local Sim
Matches 251;
     SEQUENCE
                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-3721357; PubMed-9097039;
Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasal H., Rashimoto K., Kinura S., Kitakawa M., Kitagawa M., Kasal M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28.0-40.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94100243; PubMed-8274505;
Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
"An Escherichia coli gene showing a potential ancestral relationship to the genes for the mitochondrial import site proteins ISP42 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Alley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                 Bacteria, Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISP42 AND MOM38.
-!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
992 SQKEGNLTISSDKINITKQITIKKGIDGEDSSSDATSNA 1030
                    YDEK_ECOLI STANDARD; PRT; 1325 AA. P32051; P76140; P77168; Ol-OCT-1993 (Rel. 27, Created) Ol-NOV-1997 (Rel. 35, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Hypothetical lipoprotein ydek precursor (ORFT). YDEK OR ORFT OR B1510.
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EcoGene; EG11780; ydeK.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
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D90794; BAA15197.1; ALT_INIT.
X73295; CAA51730.1; ALT_FRAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000248; AAC74583.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res. 3:363-377(1996).
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    Escherichia coli
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74;
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Matches 326; Conservative 202; Mismatches 544; Indels 431; Gaps
                                                                                                                                                                                                                                                                                                             61 SIPQSVLASGLQGMDVVHGTATMQVDGNK+TIIRNSV--DA-IINWKQFNIDQNEMVQFL 116
                                                                                                                                                                                                                                                                                                                                                                                                                       97 AGGNAS-----LITITISVIGANEDSEGTV-------NVLGGTWRLYDSGN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 ---NARPLNVGQSGTGTL-NIKQKGHV----DGGXLRLGSSTGGVGTVNVEG----- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 ----EDSVLTTELFEIGSYGTGSLNITD----KGYVTSSIVAILGYQAGSNGQVVVEKG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 QENNNSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISN 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 ENIKARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 QKITISDIINPIITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKS 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 GNIVLSAKE------GEAEI--GGVISAQNQQAKGGKLMITGDKVTLKTGAVID 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           343 LSGKEGGETYLGGDERGEGKNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWGDIALIDGN 402
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                                                                                                                                                                                                                                      1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
                                                                                                                                                                                                                                                                                                                                   458 GINDEFP-TGTGEASDPKKNSELKTTLTNTTISNYLKNAWTMNITASRKLTV--NSSINI 514
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                                                                                                                                                                                                                                                             629 THNL----SGTINISGNITINQT-----TRKNTSYMQTSHDSHWNVSALNLETGANFT 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      678 FIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIR 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         546 -LKTSSTNAQLLQV------GVLGTGELNITTGGIVKAR------DTQIALNDK 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L-----TIN-----ATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLG 839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 441.5; DB 1; Length 1325;
                                                       19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.
19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
884 N-> K (IN REF. 3).
1317 1317 M -> S (IN REF. 3).
1325 Aa; 136514 MW; 26A3A066FA19AD7D CRC64;
Hypothetical protein; Membrane; Lipoprotein; Signal;
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1325
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                     Complete proteome.
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1037 GQNDYQGATYVQMGTLRTDADGALGNTRELNISNAAIVDLNGS-----TQTVETFTGQM 1090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1143 ITASEKVTTTAGSTINATNGKASITTKTGDISGTISGNTVSVSATVDLTTKSGSKIEAKS 1202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1261 GSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVAGSDIKATSGTLVINAKDAK 1320
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                                                                                                                                                                                                                           793 TGTEFAGVAQLKDSTFTLERDNTAALTHAMLQ-------SDSENTTSVK 834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              891 GDVLID------VPKPWNDPMANNPLTTLNLLEHDDSHVGVQLVKAQTVIGSGGSLTLR 943
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
0uter membrane protein B precursor (168 KDa surface-layer protein)
(Surface protein antigen) (Cell surface antigen 5) (Sca5) (Tomp8)
(romp B) [Contains: 120 KDa surface-exposed protein (Surface protein antigen) (L10 KDa outer membrane protein omp8); 32 KDa beta peptidel.
                                                                                   684 GYQVDMLITGD---DKDGKVIHDAGHTVFNAGNTYS-----GKTLVNDGLLTIASHT 732
840 GONSSSSITGNITIEKAANVTLEAN----NAPNOONIRDRVIKLGSLLVN-GSLSLTGEN 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92167802; PubMed-1724278; Galmore R. D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.; Calmore R. D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.; The 120 kilodalton outer membrane protein (romp B) of Rickstsia rickettsii is encoded by an unusually long open reading frame: woldence for protein processing from a large precursor."; Mol. Microbiol. 5:2361-2370(1991).
                                                                                                                                                                                                                                                                                                                                            936 -----GVVKLGNVTNDGDLNIT---THAKRNQRSIIGGDIINKKGSLNITDSNNDAEIQ
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                                                                                                                                                                      895 ADIKGNLTISESATFKGKTRDTL---NITGNFT----NNGTAEINITQ---
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             467 GVVQLSGTHAAELRLGNAGSIFKLADGTVINGKVNQTALVGGALAAGTITLDGSATITGD 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              356 DERGECK-NGIQLAKKTSLEKGSTINVSGKEKG----GFAIVW--GDIALIDGNI---- 403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 FLINPNGITIGKDAIINTNGFTASTLDISNENIKARNFTFEQTKDKALAEIVNHGLITVG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 -----AVTVSED---TTLGF----ITNVVHNAHSFNLTLNAGKTL-----TIT 136
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Pfan; PF02708; rOmpA_rompB; 1.
Pfan; S-layer; Cell wall.
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MEDLINE=90136087; PubMed=2515418;
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538 ITSKGG-----NLTIYSGGWVDVHKNITLDQGFLNITAA-----SVAFEGGNNKARDAAN 587
                                                                                          ----AQGTVTITGEGKDFRANNVSLNGTGKGLNIISSVN 626
                                                                                                                                                                                                                   633 -----SKTVLSNGNVAINELVIGNDGAVQFAHDTYLITRTTNAAGQGKIIFNPVVNNGT 686
                                                                                                                                                                                                                                                                687 ----KGLTTQYRSSAGVNF--NGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFL 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----RESNSDNDTGLTITAKNVEVNKDI 1135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1053 STSMIGTTKANNGTVTYLGNAFVGNIGDSDTPVASVRFTGSDSGAGL-----QGNIYSQV 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSLKTVNITASEKVTTTAGSTINATNGKASITTKTGDI-SGTIS-GNTVSVSATVDLTTK 1193
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                                                                                                                                                                                                                                                                                                                                                      740 ANITATGG--GSVFFDIYANHSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLT 797
                                                                                                                                                                                                                                                                                                                                                                                         728 TNITTIDANVGSFVFN------AGGTNI-VSGTVGGQQGNKENIVAL 767
                                                                                                                                                                                                                                                                                                                                                                                                                                          798 INATUSNESLRQTKDDFYDGYARNAINSTYNISILGGNVTLGGQNSSSSI-----TGN 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    768 ENGITVKFLGNAT----FNGNTTIAANSTLQI----GGNYTADCVASADGTGIVEFVNTGP 820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  851 ITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLVNGSLSLTGENADIKGNLTISE---SA 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            821 IT-----VTLNKQAAP-----VNALKQITVSG-------PGNVVINEIGNAG 855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              856 NHHGAVIDTIAFENSSLGAVVFLPRGIPFNDAGNIMPLTIKSTVGNKTAKGFDVPSVVVL 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G--NVTNDGDLNITTHAKRNQRSIIG-----GDIINKK-----GSLNITDSNNDAEI 985
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                                         527 IGNAGGAAALQRITLAN----DAKKTLTL--GGANIIGAGGGTIDLQANGGTIKLTSTQN
                                                                                                                                581 NIVVDFDLAIATDQTGVVDASSLTNAQ-TLTINGKIGTIGANNKTLG----QFNIGS---
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AC P25927; P25928; Q9XCQ3;
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PRT; 1953 AA.

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                                                                                                                                                                                                                                STRAIN-LT2 / SGSC1412 / ATCC 700720;
MCDLINE-215348; PubMed=1167769;
MCDLalland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulyaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Bacteriol. 173:325-333(1991).
-!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
in positions 414 and 732.
                                                                                                                                                                                                                                                                                                   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91100301; PubMed=1987123; Wu J.Y., Siegel L.M., Kredich N.M.; "High-level expression of Escherichia coli NADPH-sulfite reductase: requirement for a cloned cysG plasmid to overcome limiting stroheme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUTATIVE SURFACE-EXPOSED VIRULENCE PROPER BIGA.

15 X 11 AA TANDEM REPEATS.

1 (INCOMPLETE).

2 (INCOMPLETE).

4 .

5.
                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
01-MAY-1992 (Rel. 22, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative surface-exposed virulence protein biga precursor.
BIGA OR STM3478.
                                                                                                                                                  STRAIN=ATCC 14028;
Stojiljkovic I., Valentine P., Heffron F.;
"Salmonella typhimurium rhs homolog.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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EMBL; M64606; AAA27043.1; ALT_FRAME.
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PIR; D39200; D39200.
StyGene; SG10437; bigA.
Virulence; Repeat; Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                          Nature 413:852-856(2001).
                                                                    Salmonella typhimurium
                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                           NCBI_TaxID=602;
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1459 NGEINLLCDSGCDIXAPGTTGTQ-----NDHNGTADIVIPDATTAPTEGSIPTPPADPN 1512
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                                                                                                                                                                                                                                                                  1185 GASLTVNGTVTINGGANALANYGTLDADAISTWHSLFNEADGSITTDLLTLNG----- 1237
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16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

OUTER membrane protein B precursor (168 kbs surface-layer protein)

(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)

(rOmp B) (Contains: 120 kbs surface-exposed protein (Surface protein antigen) (120 kbs outer membrane protein ompB); 32 kbs beta peptide).

OMPB OR RC1085.
                                                                                                 1066 QADELVGMAALNGGVVINDISGVINIDADYGQAFLSDSSSYIINNGSINLNGSPMDDTDS 1125
                                                                                                                                           962 IIGGDIINK-----KGSLNITDSNNDABIQIGGNISQKEGNLTISSD------ 1003
                                                                                                                                                                                     1126 HMGGTPTDKIWIQSLPGSGDSDTRTSDTGFFTAGTLA-NYGTETLNGDVDVNGGWLYNEA 1184
                                                                                                                                                                                                                             1004 --KINITKQITIKKGIDGEDS----SSDATSNANLTIKTKELKLTED-LSISGFNKAEIT 1056
1035 -----NNAG----DGVTG 1065
                                                         915 DTLNITGNFINNGTAEINITQGVVKL-------GNVTNDGDLNITTHAKRNQRS 961
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BEDLINE-21442074; PubMed-11557893;
Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79;
                                                                                                                                                                                                                                                                Stenos J., Walker D.;
"The rickettsial outer membrane protein A and B genes of Rickettsia australis, the most divergent rickettsia of the spotted fever group."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

-- FUNCTION: THE LIO KDA SURRACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
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120 FACE - EXPOSED PROTEIN.
32 KDA BETA PEPTIDE.
6 -> A (IN STRAIN INDIAN TICK TYPHUS).
7 K -> N (IN STRAIN INDIAN TICK TYPHUS).
7 K -> N (IN STRAIN INDIAN TICK TYPHUS).
8 -> A (IN STRAIN INDIAN TICK TYPHUS).
9 -> V (IN STRAIN INDIAN TICK TYPHUS).
1 -> V (IN STRAIN INDIAN TICK TYPHUS).
8 -> L (IN STRAIN INDIAN TICK TYPHUS).
8 -> L (IN STRAIN INDIAN TICK TYPHUS).
9 C -> GH (IN REF. 3).
1 E -> S (IN REF. 3).
1 C -> S (IN REF. 3).
1 C -> S (IN REF. 3).
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1 C -> S (IN REF. 3).
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                                   "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).
                                                                                                                                                        Phylogenetic analysis of members of the genus Rickettsia using the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 SEKPARMKVRHLALKPLSAMLLSLG----VTSIPQSVLASGLQGMDVVHGTATMQVDG-- 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AQKPNFLK-----KLISAGLVTASTATIVASFAGSAMGAALQQNRTINAVAT-TVDGVG 54
Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 194; Mismatches 617; Indels 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 1655;
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                                                                                                                                                                           gene coding the outer-membrane protein rompB (ompB).";
Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
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                                                                                                      STRAIN-Indian tick typhus, and Malish 7;
MEDLINE-20393643; PubMed-10939649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.8%; Score 428;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred.
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EMBL; AF123721; AAF34124.1; -
EMBL; AF123726; AAF34129.1; -
                                                                                     SEQUENCE OF 33-1649 FROM N.A.
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                                                                                                                                           Roux V., Raoult D.;
                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY)
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les 348; Conserv
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----- IGKDAIINTN---- 165
                             -----GFTASTLDISNENIKARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGG--K 217
                                                                                                                                               172 VGRIDCGAAASTLVFNLAN-----PTTQKAPLILGDNAVIVNGANGTLNVTNGFIK 222
                                                                                                                                                                                              218 VKNEGVISVNGGSISLLAGQKITISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRA 277
                                                                                                                                                                                                                                 278 ATIRNQGKLSADSVSKDKSGNIVLSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKT 337
                                                                                                                                                                                                                                                                                                                                                                                                     338 GAVI-DLSGKEGGETYLGGDERGEGKNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWGDI 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIDGNINAQGSGDIAKTGGFV-ETSGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFN 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 VAVNGOLKANAGANAAVIGTNNGAGR---AAGFVVSVDNGKVATIDGOVYAKDMVIQSAN 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456 NTGINDEFPTGTGEASDPKKNSELKTTLTNTTISNYLKNAMTMNITASRKLTVNSSINIG 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 TMTLNGNF---TGDASNPGNTAGVITFDANGTLASASADA---NVAVTNNITAIEASGAG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       570 ----AASVAFEGGNNKARDAANAKIVAQGTVTITGEGK----DFRANNVSLNGTGKGLNII 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       526 DIGNACGAAALQCITLANDA--TKTLTLGGANIIGANGGTINFOANGGTIKLTSTQNNIV 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584 VDFDLAIATDQTGVVDASSLTNAQTLTINGKIGTVGANNKTLGQFNIGSSKTVLSDGDVA 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       758 HSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDG 817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       745 -------AGGTNI-VSGTVGGQGGNKFNTVALDNGTTVKFLGNAT----FNG 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           871 NIRDRVIKLGSLLVNGSLSLTGENADIKGNLTISE---SATFKGKTRDTL----- 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----VNALKQITVSG------PGNVINEIGNAGNYHGAVTDTIAFENSSLGAV 876
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                                                                                                                                                                                                                                                                                                                                                  261 ATITFNG------TDGTGRLVLLSKNAAATDFNVTGSLGGNLKG------IIEFNT
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NRVISNQISQLKGILDSNGQVFLINPNGIT----
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                                                                                 1170 TGDI-SGTIS-GNTVSVSATVDLTTKS-GSKIEAKSGEANVTSATGTIGGTISGNTVNVT 1226
                                                                                                                                                                                                                   1227 ANA-----GDLT---VGNGAEINATEGAATLTATGNTLTTEAGSSITSTKGQVDLLAQNG 1278
                                                                                                                                                                                                                                                          1194 DNANANFSGTOTYTLIQGGARFNGTLGGPNFVVT-----GSNRFVNYGLIRAANODY 1245
                                                                                                                                                                                                                                                                                               1279 SIAGSINAANVTLNTTGTLTTVAGSDIKATSG-----TLVINAKDAKLNGD---ASGDST 1330
                                                                                                                                                                                                                                                                                                                                  1246 VITRTNNAENVVTN-----DIANSSFGGAPGVGQNVTTFVNATNTAAYNNLLLAKNSAN 1299
                                                                                                                                                                                                                                                                                                                                                                              1331 EVNAVNASGSGSVTAATSSSVNITGDL----NTVNGLNIISKDGRNTVRLRGKEIEVKY 1385
                                                                                                                                                                                                                                                                                                                                                                                                                 1300 SANFVGAIVTDTSAAITNAQLDVAKDIQAQLGNRLGALRYLGTP--ETAEMAGPEAGA-- 1355
1045 RFVDG-ILSHSTSMIGTTKANNGTVTYLGNAFVGNIGDSD-----TPVASVRFTGSD 1095
                                                         1110 GGRESNSDNDTGLTITAKNVEVNKDITSLKTVNITASEKVTTTAGSTINATNGKASITTK 1169
                                                                                                                                                                           1142 TLTFASGTSTWGNNTSIETTLTLANGNIGNIVILEGAQVNATT-TGT-----TTIKVQ 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIATION (1988) PubMed=3290200;
Poole K., Schiebel E., Braun V.;
"Molecular characterization of the hemolysin determinant of Serratia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
SUBJECTIOLAR LOCATION: Outer membrane.
SUBJECTIOLAR LOCATION: Outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. BECLETIOI. 170:3177-3188(1988).
-!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serratia marcescens.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
NOV-1990 (Rel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND SEQUENCE OF 31-40
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644 DINLTLVSHKDADVIG--SQVASGGELSVESKTGNI--NVKAAER------QQNIDEQK 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   673 GANFTEIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSK 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              733 PLPIRFLANITATGGGSVFFDIYANHSG---RGAELKMSEINISNGANFTLNSHVR---G 786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              693 -----TALTVNG----YAKEAGDKQYRAGLRIEHTRDSEKTTRTENSASSLSGG 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264 I------INTAQGSGVKLAGSINAGDELKVKAYDIRSESRV--DDASSNKNGGDN 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 INAQGSGDIAKTGGFVETSGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDE 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  463 FPTGTGEASDPKKNSELKTTLTNTTISNYLKNAWTMNITASRKLTVNSSINIG--SNSHL 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 ---FEQTKDKALAEIVN--HGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 VODFKOSNGKVTSAAINAISGLNRVARDGTV----QASQQMPTALDSYYLGSMQAGRIN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 300
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                                                                                                                                                                                                                                                                                                                                  89 LSQLAGQLGANPNLGGREASVILNEVIGRNPSLLHGQQEIFGMAADYVLANPNGISCQSC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                149 GFINTSHSSLVVGNPLVENGVLOGYSTFGNRNTLSLNGTLNAGGVLDLIAPKIDSRGEVI 208
                                                                                                                                                                                            62 IPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQ------- 109
                                                                                                                                                                                                                                                                                     110 -NEMVQFLQENNN-----SAVFNRVTSNQISQLKG---ILDSNGQVFLINPNGITIGKD 159
Query Match
5.7%; Score 425; DB 1; Length 1608;
Best Local Similarity 21.0%; Pred. No. 2.4e-10;
Matches 351; Conservative 216; Mismatches 576; Indels 528; Gaps
                                                                                              2 NKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVTS 61
                                                                                                                                             3 NNNFRLSAAGKLAAALAIILAASAGAYAAE---------IVAANGANG 41
                                                                                                                                                                                                                                      42 PGVSTAATGAQVVDIV-----APNGN-GLSHN-----QYQDFNVNQPGAVLNNSREAG 88
                                                                                                                                                                                                                                                                                                                                                                                      160 AIINT-------NGFTASTLDISNENIKARNFT------
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959 QRSIIGGDI-----INKKGSLNITDSNNDAEIQIGG----NISQKEGNLTISS 1002
                                                                                                                                                     1003 DKINITKQ-----ITIKKGIDGEDSSSDATSNA-NLTIKTKELKLTEDLSISG 1049
                                                                                                                                                                                                                                          1050 FNKAEITAKDGRDLTIGNSNDGNSGAEAKTVTFNNVKDSKISADGHNVTLNSKVKTSSSN 1109
                                                                                                                                                                                                                                                                                   985 ANRODEQSRDTR-----GSAGVRYYTTT------GSDLTVDAK----GEG 1019
                                                                                                                                                                                                                                                                                                                               1110 GGRESNSDNDTGLT----ITAKNVEVNKDITSLKTVNITASEKVTTTAGSTINATNGKA 1164
                                                                                                                                                                                                                                                                                                                                                                        1020 GTQRSNSSASQAVTGSIDAANGINVNVKKD-------AIYQGTALNGGRGKT 1064
                                                                                                                                                                                                                                                                                                                                                                                                                 1165 SITTKTGDI-----SGTISGNTVSVSATVDLTTKSGSKIEAKSGBANVTSATGTIG 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1216 GTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEAGSSITSTKGQVDLLA 1275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1156 -----SLSAGNKVALQAAESTQT-------RKESKLSGNIDLGAGSSDS 1192
1330 TEVNAVNASGSGS--VTAATSSSVNITGDLNTVNGLNIISKDGRNTVRLRGKEIEVKYIQ 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1193 KEKTGGNLSAGGAFDLAKVNESATERQG-----ATIASDGKVTLSANGKGDDALHLQ 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1388 PG-VASVEEVIEAKR---VLEKVKDLSDEERETLAKLGVSAVR-------FVEPN 1431
                                                                                                         876 VGVNIGANVDYSAVTRPVERAVGKAAKLDATGVIND----IGGIGAPNVGLDIGAQGGSS 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1245 GAKVSGGSAALEAKNGGILLESAK---NEQHKDNWSLGIKANAKGGQTFNKDAGGKVDPN 1301
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OSSOIO (92CO).

OSSOIO (ARL. 39, Created)

30-MAY-2000 (Rel. 39, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

15-JUN-2002 (Rel. 41, Last annotation update)

Outer membrane protein B precursor (168 kDa surface-layer protein)

(Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)

(TOMP B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91045972; PubMed=2122457; Carl M., Dasch G.A.; Carl M., Dobson M.E., Ching W.M., Dasch G.A.; Carl M., Dobson M.E., Ching W.M., Dasch G.A.; Ching the protective paracrystalline-surface-layer protein of Rickettsia prowazekii: presence of a truncated identical homolog in Rickettsia typhi."; Proc. Natl. Acad. Sci. U.S.A. 87:8237-8241(1990).
                                                                                                                                                                                                EKRSSSSQAVVSSVQAGSIDINAKGEVRDQGTQYQASKGAVNLTADSHR-----SEAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1302 TGKDTHTLGAGLKVGVEQQDKTTHANTG--ITAGDVTLNSGKDTRLAGARV 1350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBI_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            Hackstadt T., Messer R., Cleplak W. Jr., Peacock M.G.;
"Evidence for proteolytic Cleblak W. Jr., Peacock M.G.;
"Evidence for proteolytic Clebavage of the 120-kilodalton outer membrane protein of rickettsiae: identification of an avirulent mutant deficient in processing.";

In Function: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STROTURENE PROTEIN WHICH MAY PLAY A ROLE AS A RICKETISIAL VIRULENCE FACTOR AND/OR IMMUNGEN DURING INFECTION.

I- FUNCTION: THE 32 kDa BETA PEPPIDE MAY SERVE AS A MEMBRANE ANCHOR.

I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAVER WITH HEXAGONAL SYMMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTOEAPLTICA -> INSRSSSYHLVS (IN REF. 1).
T -> I (IN REF. 1).
Q -> L (IN REF. 1).
D -> G (IN REF. 2).
T -> S (IN REF. 2).
W; 735FDF392E6346CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 LALKP-LSAMLLSLGVTSIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 QFNIDQ-----NEMYQFLQENNNSAVFNRVTSNQISQLKGILDSNGQVFLINPN- 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 218; Mismatches 585; Indels 464; Gaps
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                                                                                                  Andersson S.G.E., Zomorodipour A., Andersson J.O., Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K., Eriksson A.-S., Winkler H.H., Kurland C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                         of
                                                                                                                                                                                                                                                                              Ching W.M., Carl M., Dasch G.A., "Mapping of monoclonal antibody binding sites on CNBr fragments the S-layer protein antigens of Rickettsia typhi and Rickettsia prowazekii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPRUUsesu, TompB; 1.
Pfam; PF02708; rOmpA_rOmpB; 1.
Antiqen; S-layer; Cell wall; Complete proteome.
120 KDA SURPACE-EXPOSED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
"Sequence analysis of ompB of Rickettsia prowazekii.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V -> A (IN STRAIN BREINL).
Y -> D (IN STRAIN BREINL).
A -> S (IN STRAIN BREINL).
AA -> VC (IN REF. 1).
TTQEAPLILGA -> INSRSSSYHLVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M37647; AAA26390.1; ALT_INIT.
                                                                     STRAIN-Madrid E;
MEDLINE-99039499; PubMed-9823893;
                                                                                                                                                                                                                                           STRAIN=Breinl;
MEDLINE=92114896; PubMed=1370573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF161079; AAD42234.1; -- EMBL; AJ235273; CAA15140.1; -- InterPro; IPR003858; rOmpA_rOmpB.
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-92104668; PubMed-1729180;
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                                                                                                                                                                                                                                                                                                                                                 Mol. Immunol. 29:95-105(1992).
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                                                                                                                                                                                            Nature 396:133-140(1998).
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1643
257
1010
1450
179
201
212
313
1104
                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                           PARTIAL SEQUENCE.
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                                                                                                                                                                           mitochondria.
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86	211	148	265	205	293	330	324	376	383	426	436	486	472	543	527	009	119	638	636	688	682	745	720	805	176	847	835	899	875	946	930		977	1055
	9-		NLIGGKVKNEGVISVNGGSISLLAGGKITISDIINPTI			VNGGNGTLNITNGFIQVSDNIFAGIKI	DESCRIPTION   DESCRIPTION			STINVSGKEKGGFAIVWGDIALIDGNIN		IKDNAIVDAKEWLLDFDNV :  :		TISNY-LKNAWTMNIT	3 HIAELRIGNGGSIFKLADGTVINGPVNQNALMNNALAAGSIOLDGSAIITGDIG	NLTIYSGGWVDVHKNITLDQG		1 EGKDFRANNVSLNGTGKGLNIISSVNNLTHNLSGTINII	TONNIVVNFDLDITTDKTGV-VDASSLTNNQTLT	9SGNITINQTTRKNTSYWQTSHDSHWNVSALNLETGANFTFIKYISSNSKG	LNAGDVAINELVIENNGSVQLNHNTYLITKTINAAN	9 LTTQYRSSAGVNFNGVNGNMSFNLKEG		ASSSS	GKG		7 LGDTTFNGGTKIEGKSILQISNNYTTDHVESADN-TGTLEFVNTDPITVTLNKQGAYFGV	TGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLVNGS	6 LKQVIISGPGNIVFNEIGNVGIVHGIAANSISFENASLGT	O NLTISESATFKGKTRDTLNITGNFT-NNGTABINITQGVVKLGNVTND	SLFLPSGTPLDVLTIKS	47GDENITTHAKRNQRSIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKEGN	31 LSLGSDNSITVNANTLYSGIRTTKNNQGTVTLSGGMPNNPGTIYGLG	18 LTISSDKINITKQITIKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAEI 
54	153	66	212	149	266	206	266	333	325	377	384	427	437	487	473	544	528	601	578	639	637	683	683	746	721	806	777	848	836	900	876	94	93.	66
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	NIAEQDKKGGIAGYKAKTTGV	1369	рр
	1333 NAVNASGSGSVTAATSSSVNITGDLNIVNGLNII 1366	133	Qy
1368		1309	qq
1332	7 LTTVAGSDIKATSGTLVINAKDAKLNGDASGDSTEV	1297	Qγ
1308	VYTTAVGNSAIANAPGVSQNISRCLESTNTAAYNNM	1250	οqα
1296		1255	Qγ
1249	O ANANFSGTQAYTLIQGGARFNGTLGAPNFAVTGSNIFVKYELIRDSNQDYVLTRTNDVLN	1190	QQ
1254		1222	δλ
1189	:	1131	qq
1221		1165	Qy
1130		1079	qq
1164	2RESNSDNDTGLTITAKNVEVNKDITSLKTVNITASEKVTTTAGSTINATNGKA	1112	Qy
1078		1024	qq
1111	6 TAKDGRDLTIGNSNDGNSGAEAKTVTFNNVKDSKISADGHNVTLNSKVKTSSSNGG	1056	δ
1023	8 LENGSPKLKQVTFTTDYNNLGSIIANNVTINDYVTLTTGGIAGTDF 1023	978	qq

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I MNKIYRLKFSKRLNALVAVS......CFSSGNGARVCTNVADDGQP 1477
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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2: Sp_bacteria:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q48028 haemophilus	Q48031 haemophilus	Q9rni2 haemophilus	Q93dc7 yersinia en	Q8zby3 yersinia pe	Q8xq42 ralstonia s	Q9hvg6 pseudomonas	Q9hvn6 pseudomonas	Q8zhal yersinia pe	Q9f285 yersinia pe	Q9zhl0 haemophilus	Q8xpu7 ralstonia s	Q9hwu6 pseudomonas	Q98e20 rhizobium l	Q8rdq9 fusobacteri	Q8rip5 fusobacteri
SUMMARIES	1																
SUMM	ID	048028	048031	Q9RNI2	Q93DC7	Q8ZBY3	Q8 XQ4 2	99AH60	9NAH60	Q8ZHA1	Q9F285	OSTHLO	Q8XPU7	90WH60	Q98E20	Q8RDQ9	Q8RIP5
	DB	7	7	7	7	16	16	16	16	16	7	7	16	16	16	16	16
	Match Length DB	1477	1536	1557	2065	1910	1371	2154	1417	3705	3705	4919	2737	1018	3930	3165	2143
% 21012	Match	98.8	6.99	63.6	12.2	11.8	10.6	10.1	9.8	8.1	8.0	8.0	7.6	7.5	7.4	7.3	7.3
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                                      LNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVNGLNIISKDGRNTVRLRGKE 1380
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                        KSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEA
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Matches 1046; Conservative 146; Mismatches 265; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Infect. Immun. 60:1302-1313(1992).
EMBL; U08876; AAA20527.1; -.
InterPro: IPR000169; SHPOT_acsite.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN.1.
SEQUENCE 1536 AA; 159916 MW; 5CA1C31F9DCF188E CRC64;
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Last annotation update)
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MEDLINE=92192797; PubMed=1548058;
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                                         540 ----SKGGNLTIYSGGWVDVHKNITLD-QGFLNITA-ASVAFEGGNNKARDAANAKIVAQ 593
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                              301 LSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGE 360
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                                                                1362 GLNIISKDGRNTVRLRGKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLG 1421
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1302 GSDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVN 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.6%; Score 4711; DB 2; Length 1557;
63.3%; Pred. No. 2.3e-146;
ive 155; Mismatches 290; Indels 136; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 SIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-20359363; PubMed-10899870; van Schilfgaarde M., van Ulsen P., Eijk P., Brand M., Stam M., kouame J., van Alphen L., Dankert J.; "Characterization of adherence of nontypeable Haemophilus influenzae to human epithelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
                                                                                                                                 1422 VSAVREVEPNNTITVNTQNEFTTRPSSQVIISEGKACFSSGNGARVCTNVADDGQ 1476
                                                                                                                                                    1482 VSAVRFIEPNNTITVDTQNEFATRPLSRIVISEGRACFSNSDGATVCVNIADNGR 1536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Schilfgaarde M., Eijk P., Van Ulsen P.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF180944; AAD56660.1; -
InterPro; IPR000169; SHProt_acsite.
PROSITE: PS00639; THIOL_ENGTEASE_HIS; UNKNOWN.1.
SEQUENCE IS57 AA, 160461 MW; 62524D384398CB37 CRC64;
                                                                                                                                                                                                                                                                                      01.MAY-2000 (TrEMBLrel. 13, Created)
01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.HAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                     PRT; 1557 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to human epithelial cells.";
Infect. Immun. 68:4658-4665(2000).
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Conservative 155;
                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                        Haemophilus influenzae.
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          421 SGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDEFPTGTGEASDPKK-NSEL 479
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                                                                                    480 KITLINITISNYLKNAWIMNITASRKLIVNSSINIGSNSHLILHSKGQRGGGVQIDGDIT 539
                                                                                                 S-KGGNLTIYSGGWVDVHKNITLDQGFLNITA-ASVAFE-GGNNKARDAANAKIVAQGTV 596
                                                                                                                                           653
                                                                                                                                                                                                                     654 YWQTSHDSHWNVSALNLETGANF--TFIK-----YISSNSKGLTTQYRSSAGVNFNGV 704
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                                                                                                                                                                         597 TITGEGKDFRANNVSLNGTGKGLNIIS---SVNNLTHNLSGTINISGNITINQTTRKNTS
                                                                                                                                                                                       RGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYAR
                                                                                                                                                                                                                                                                                                                        705 NGNMSFNLKEGAKVNFKLK-PNENMNTSKPLPIRFLANITATGGGSV---FFDIYANHSG
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81;
               1393 VEEVIEAKRVLEKVKDLSDEERETLAKLGVSAVRFVEPNNTITVNTQNEFTTRPSSQVII 1452
NAVNASGSGSVTAATSSSVNITGDLNTVNGLNIISKDGRNTVRLRGKEIEVKYIQPGVAS 1392
                                                                                Query Match 12.2%; Score 900; DB 2; Length 2065; Best Local Similarity 25.0%; Pred. No. 7.8e-22; Matches 420; Conservative 258; Mismatches 623; Indels 378; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 PLSAMLLSLGVTSIPQSVLAS---GLQGMDVVHGTATMQVDGNK-TIIRNSVDAIINWKQ 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 VINTPQGKVALASGSRVILNLDRGNLLGVQV-----QGEQVNTLLQNGGLIRADEGVI 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         274 NVRA------ATIRNQGKLSADSVSKDKSGNIVLS-AKEGEAEIGGVISAQNQQAKGG 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : || |::| : || 398 THQGAGGTAVLWSEHYTGFYGDIHARG-GSLSGDGGQVETSSQRNLQSFGRVDVSAIMGN 456
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Infect. Immun. 69:6201-6208(2001).

Interpro: IPRO011950; TIF_SUII.
PROSITE: PS01118; SUII.1. UNKNOWN.1.

SEQUENCE 2065 AA: 210024 MW; A306D07636B2D176 CRC64;
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                                                                                                                                                 1453 SEGKACFSSGNGARVCTNVADDGQ 1476
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                                                                                                                                                                                                                                                    PRELIMINARY;
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1340 KGSSVAGSGVAISGMVNNSSGPVTIEGSSTDGSGVHLFSAEHQINRINVTGSSTQAEGLR 1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            942 NVTNDGDLNITTHAKRNQRSI-IGGDIIN---KKGSLNITDSNNDAEIQIGGNISQKEGN 997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            776 ANF---TLNSHVRGDDAFKI---NKDLTIN-AINSNFSLRQTKDDFYDGYARNAINSTY- 827
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                                   457 TGRWLLDPAEVNIVGSGAESGVSVQIG---DIPAGYVKNAQVFTPMAN---VTQILNTSI 510
                                                                                                                           638 ISG-NITINQ------TTRKNTSYWQTSHD-SHWNVSALN--LETGANFTFI 679
                                                                                                                                                                                                                                                                                                                                                                                                              659 ISGESSNANQQGWRGIDISGDSVFAGKGNMSFTMTSNSRSSWMGTFTNATIAGDKNITF- 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    680 KYISSNSKGLTTQYRSSAGVNF-NG----VNGNMSFNLK-------EGAKVNFK 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              770 ---NVNVEINTKGVDGFLLRDSHITATAG-----NISANATTTHKGLWISGDTDLNASKN 821
435 AKEWLLDFDNVSI----NAEDPLFNNTGINDEFPTG---TGEASDPKKNSELKTTLTNTTI 488
                                                                                             489 SNYLKNAWTMNITASR-----KLTVNSSIN--IGSNSHLILHSKGQRGGGVQIDGD 537
                                                                                                                                                                                     538 ITSKGGNLTIYSGGWVDVHKNITLDQG-----FLNITAASVAFEGG------NNKA 582
                                                                                                                                                                                                                                   561 IVSNGHNITATTG-----KLNLNLLSGDSIVDSIITLNNSDVLLNGGDLLMKHANENNAA 615
                                                                                                                                                                                                                                                                               583 RDAANAKIVAQGTVTITGEGKDFRANNVSLNG-TGK----GLNIISSVNNLTHNLSGTIN 637
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395 DIALIDGNINAGG---SGDIAKTGGFVETSGH---DLFIKDNAIV---DAKEWLLDFDNV 445
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MEDLINE-21470413; PubMed=11566360;
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamiln N., Holroyd S., Jagels K., Karlyshev A.V.,
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Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
Genome Sequence of Frefaina pestis, the causative agent of plague.?,
Nature 413:523-527(2001).
BABUS, AJ441565 (AC92482.1;
Hypothetical protein; Complete proteome.
ERQUENCE 1910 AA; 195076 MW, C6E5127A098E4045 CRC64;
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                          tch 11.8%; Score 876; DB 16; Length 1910;
bl Similarity 25.5%; Pred. No. 4.3e-21;
421; Conservative 235; Mismatches 665; Indels 332; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 IPQSVLASGLQGMD--VVHGTATMQVDGNKTIIRNSVDAI-INWKQFNIDQNEMVQFLQE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 FPLLVLAHPVLPVNGHVVIGQGMLDQQSSTLTVTQQTDKLAINWDSFDIAHGHSVIYAQP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 NNNSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNEN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 IKARNETFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNE--GVISVNGGSISLLAG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            237 QKITIS----DIINPTITYSIAAPENEAV-----NLGDIFAKGGNINVRA-----AT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 HSVTLNLDHGNLLGVQI-----QGETVAALIQNGGLIQADGGVIQLTAKGKDMLMDTV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 IRNQGKLSADSVSKDKSGNIVL-SAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTG 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339 AVIDLSGKEGGETYL-GGDERGEGKNGIQLAKKTSLEKGSTINVSGKEK--GGFAIVWG- 394
                                                                                                            1425 VRFVEP-----NNT-----ITVNTQNEFTTRPSSQVIISEGKACFSSGNGARVCTN 1470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 NKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVTS 61
                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                         01.MAR-2002 (TrEMBLrel. 20, Created)
01.MAR-2002 (TrEMBLrel. 20, Last sequence update)
01.HAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                PRT; 1910 AA.
                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     Putative adhesin.
HMWA OR YPO3247.
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                              Yersinia pestis
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ag :	413	DYTG
g c	446	b SI**NAEDPLENNYG-INDEFPTGTGEASDPKKNSELKTTLTNTTISNYLKNAWTMNIT 501
Óγ	502	ASRKLTVNSSINIGSNSHLILHSKQQRGGGVQIDGDITSKGGNLTIYSGGWVDVHKN 55
Ω	524	4 TSNSSLTGCQWCNITVQADITKTAGADATLTLQADGNIVVNNN 566
Oy Op	559	9 ITLDQGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGT 615 
δλ	616	GKGLNIISSVNNLTHNLSGTINISGNITINQTTRKNTSYWQTSHDSHWNVSALNLET 67
QQ	614	AR-IGLLGGR
Oγ	673	GANFTFIKYISSNSKGLTTQ
QΩ	653	
Qy Dp	727	NMNTSKPLPIRFLANITATGGGSVFFDIYANHSGRG 762
Qy	763	AELKMSEINISNGANFTL-NSHVRGDDAFKINKDLTINA-TNSNFSLRO
qq	765	
δλ	810	
Q	825	TINS
g Q	850	NITIEKAANVTLEANNAPNOQNIRDRVIKLGSLLVNGSLSLTGENADIKGN 90
ò	901	T.T CECADERCK MODERN NITH NICHTANDAN LEAININE LIANG 93
6 6	935	
δy	926	KRNQRSIIGGDIINKKG-SLNITDSNNDABIQIGGNISQKEGNLTISSDKINITKQI
QQ	984	-GKDISIIAGNSKTATGPNINIENVNIETNNGNFTTNGITSTWLSGVNVSANGVDITSNS
So do	1012	TIKKGIDGEDS
3 8	1043	
g G	1095	NUGNSGAEAKTYTENNYKDSKISADGHNYTLNSKVRISSSNGGRESNSDNDTGLT 112
ò	1124	TOAKNVEVNKDITGIKTUNITTAGENTATAGEN TATATAGEN TATATAGAGEN TATATAGAGEN TATATAGAGEN TATAGA
, a	1145	SSGRNIDINGSSAGTGDVYFTNVELNATAGNVSIYAET
δλ	1184	VSATVDLTTKSGSKIEAKSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEINAT
QQ	1188	TSLNAVLSLGGNNSIKAQNGWLIGKAENTTQGAGIGFRANSSLSVDGNIILKGET 124
ογ	1244	EGAATLIATGNTLTT
οp	1243	129
οy	1295	GTLTTVAGSDIKATSGTLVINAK-DAKLNGDA-SGDSTEVNAVNASGSGSVTAA 1346
g	1300	GSLKMEGRSTSGTGINFPSSNNTLVFNGDGDTLIKGSSVAGTGAAISGVNNSTGPWTIE 1359
γo		TSSSVNITGDLNTVNGLNIISKDGRNTVRLRGKEIEVKXIQ 1387
ор	1360	GISTDGAGVHLFSAEHRIDRINVTGSSTHAEGLRISGNAAIVDTTLTGKSINGSGVKIDS 1419

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61;
1388 -PGVASVEEVIEAKRVLEK--VKDLSDEERETLAKLGVSAVRFVEPNNTIT-----VN 1437
                       A Arlat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
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B Interpro: IPR002064; DNA_POL_B.
B ROSITE; PS00116; DNA_POLYMERASE_B; UNKNOWN_1.
B PROSITE; PS00116; DNA_POLYMERASE_B; UNKNOWN_1.
B PROSITE; PS00116; DNA_POLYMERASE_B; UNKNOWN_1.
B PROSITE; PS00116; DNA_POLYMERASE_B; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 ISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIKARNFTFEQTKDK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 ALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKITISDIINPTITYS 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42 VRH-----LALKPLSAMLLSLGVTS---IPQSVLASGLQGM------------74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------NVRAATI-RNGG--KLSA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 ISAGAARTLVNNGGMIVADGGRVVLIARGLDSLSESVVNTTGVVRARTVGNNQGTIELIG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289 DSVS--KDKSGNIVLSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGK 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               347 EGGETYL-GGDERGEGKNGIQLAKKTSLEKGSTINVSG--KEKGGFAIVWG-DIALIDGN 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 10.6%; Score 785; DB 16; Length 1371; Best Local Similarity 24.2%; Pred. No. 2.88-18; Matches 365; Conservative 196; Mismatches 533; Indels 414;
                                                                                                                                                                                                                                                                                                                                 Plasmid megaplasmid.
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                             Putative hemagglutinin-related protein.
RSP1444 OR RS03099.
Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                  1438 TQNEFTTRPSSQVIISEGKACFSSGNGARVCTN 1470
                                                                                         1475 ENSNVTGTSEADLLILQGVATTGTGTGIKLNGN 1507
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MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                        01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=305;
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Q8XQ42;
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Q8XQ42
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1363 LNIISKDG 1370 : | | 1266 ADAGSPAG 1273

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INAQGSGDIAKTGGFVETSGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFN 455 	NTGINDEFPTGTGEASDPKKNSELKTTLTNTTISNYLKNAMTMNITASRKLTVNSSIN 513	IGSNSHLILHSKGQRGGGVQIDGDIT-SKGGNLTIYSGGWVDVHKNITLDQG 564 	FLNITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTGKGLNIISS 624 	VNNLTHNLSGTINISGNITINOTTRKNTSYMQTSHDSHWNVSALNLETGANFTFIKYISS 684	NSKGLTTQYRSSAGVNENGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFLA 740	NITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINA 800 ::    :	IFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGGONS 843 	SSITGNITIEKAANVTLEANNAPNQONIRDRVIKLGSLLVNGSLSLTGENADIKG-899 	SG	GNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSLNITDS 979   :   :	NNDAEIQIGGNISQKEGNLTISSDKINITKQITIKKGIDGEDSSSDATSNANLTIKTKEL 1039 	KLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTVTFNNVKDSKISADGHNVTL 1099 	NSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKDITSLKTVNITASEKVTTTAGSTINA 1159     :     :     :     :     :	TNCKASITTKTGDISGTISGNTVSVSATVDLTTKSGSKIEAKSGEANVTSATGTI 1214 	GGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEAGSSITSTK 1268 	GOVDLLAQNGSIAGSINAANVTLNTTGTLTTVAGSD	IKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVNG 1362 
INAQGSGE ::      LSANG-GA	NTGINDEF	GSNSHLI   :   SGGNVTIT	FLNITAAS  ::: TLDVSM	VNNLTHNI      AALSLQNS	NSKGLTT(    :   TSGGIAT	NITATGGGSV:::    :	TNSNFSL)   	SSSI	WGSGSGA	ARKAFWN	NNDAEIQ   GNT	KLTEDLS : : GITQSGA	NSKVKTS	TNT   GNWSISG	GGTISGN   : AGRAAAG	GOVDLL?   	IKATS   HAFSITE
403 I	456 N	514 1	565 1	625 7	685 1	741	801	844	900	941	980	1040	1100	1160	1215	1269	1305
Oy Dp	o do	ç q	Qy Db	Qy	oy Op	Oy Dp	Qy	Qy	Oy Dp	QY Dp	oy oy	Q Q	oy D	oy D	දු දු	Oy Op	Oy Dp

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534 IDGDITSK-----GGNLTIYSGGWVDVHKNITLDQGFL---NITAASVAFEGGNNKA 582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 AGKIDVSGPK-NGGDVLVSGQQVALASTASIDARGTAQGGSVRIGGDFQGRGE--LPRAK 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 KTSLEKGSTINVS--GKEKGGFAIVWGD-IALIDGNINAQGSGDIAKTGGFVETSGH-DL 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 FIKDNAIV-----DAKEWLLDFDNVSINAEDPLFNNTGINDEFPTGTGEASDPKKNSE 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   479 LKT-TLTNTTISNYLKNAWTMNITASRKLTVNSSI---NIGSNSH-LILHSKGQRGGGVQ 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 VVTGALAGGKVT-----LSASDRLSVEAPLITSNLGGASRGLELIATGP-AGAVD 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 VFLINPNGITIGKDAIINTNGFTASTLDISNENIKARNFTFEQTKDKALAEIVNHGLITV 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 GKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKITI----SDIINPTITYSIAAPENEA- 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 ---VNLGDIFAKGGNINVRA----ATIRNQGKLSADSVSKD---KSGNIVLSAKEGEAEI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 GGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSG-KEGGETYLGGDERGEGKNGIQLAK 369
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
STRAIN-ATCC 15692 / PAO1;
SCOVER C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnedle W.O., Kowalik D.J., Lagrou M., Hickey M.J., Brinkman F.S.L., Hufnedle W.O., Kowalik D.J., Lagrou M., Brody L.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Saler M.H., Hancock R.E. W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87 GNKTIIRNSVD-AIINWKQFNIDQNEMVQFLQENNNSAVFNRVTSNQISQLKGILDSNGQ 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.1%; Score 744.5; DB 16; Length 2154; ilarity 23.9%; Pred. No. 9.7e-17; Conservative 231; Mismatches 585; Indels 437; Gaps
                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004876; AEG08013.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 2154 AA; 219755 MW; 4B8ABCE6696BAOCE CRC64;
                    Ö9HVG6;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical protein PA4625.
PRT; 2154 AA.
                                                                                                                                      Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                        Pseudomonas.
NCBI_TaxID=287;
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    99VH60
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SEQUENCE FROM N.A.

STRAILMATCC 15692 / PAO1;

MEDLINE-2043737; Pubmed-10984043;

Stroyer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnaqie W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L. Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Snith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SIPQSVLASGLOGMDVVHGTATMQ--VDGNKTII-RNSVDAIINWKQFNIDQNEMVQFLQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            118 ENNNSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         178 NIKARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQ 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
8.6%; Score 636.5; DB 16; Length 1417;
Best Local Similarity 21.9%; Pred. No. 2.1e-13;
Matches 352; Conservative 238; Mismatches 523; Indels 495; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 QAPAFALPS---GATVVSGDAGFQTSTDGRHMVIDQQSHKLITNWNEFSVRADERVSFHQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 KITISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRA-----ATIRNQGKLSADSV 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 SKDKSGNIVLSAKEGEAEIGGVISAQN-----QQAKGGKLMITGDKVTLKTGAVIDLS 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 ----GGQVLMSARSADSLLKTVVNNQGTLEARTLRSAEGRIVLDGGEQGTVRVAGKQDAS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 GKEGGETYLGGDERGEGKNGIQLAK----KTSLEKGSTINVSGKEKGGFAIVWGDIALID 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               401 -GNINAQGSGDIAKTGGFVETSGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGI 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNKSYTLVWNQ-----ATGCWNVASEGTRRRSK-SGRGKALVVAGASLLGL-FC 47
                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003880; Ppantne_attach.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
Hypothetical protein; Complete proteome.
SEQUENCE 1417 AA; 139958 MW; 212C916D5A55C39D CRC64;
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                                                                                                                                                                     01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein PA4541.
                                                                                                                                           PRT; 1417 AA.
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-
1365 -- IISKDGRNTVRLRGKEIEVKYIQPG 1389
                        opportunistic pathogen.";
Nature 406:959-964(2000).
EMBL; AE004867; AAG07929.1; -.
HSSP; P22629; ISWC.
                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                              Pseudomonas
                                                                                                                                   9NVH60
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Db	360	VGQANAAGDG SGQVHVAQGPAGANASDSNGVTIVQQQP 397	
Qy	460	NDEFPTGTGEASDPKKNSELKTTLTNTTISNYLKNAWTMNITASRKLTVNSSINIGSNSH 519	
Db	398	AVDLAAGANGTSAVQSQSGANIGSGANGISVVQSQNSPNIGSGAN 442	
δλ	520	GGWVDVHKNITLDQGFLN	
QQ	443	GISVVQSQNGANIGAGASGISVVQSQNSPNIGSGVNGVTVVQSQNGANIGSGASG 497	
Oy da	568	ITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTGKGLNIISSVNN 627 	
a .			
δ d	628	LTHNLSGIINISGNITINQTTKKNISYWQISHDSHWNVSALNLEIGANFI 0//	
λõ		GVNGNMSF	
q	601		
Οy	738	FLANITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTLNSHV784	
QQ	625	- LANPSSAGKGSTLHADTLARNLSTSNVEVVATRGNAHVGAPLSWDSGNGLT 675	
Qy	785	RGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGG 840	
QQ	929	LTAERGDLRINGALTAQGENASLTLNAGQRPLRIDDSLSLTGQGARVEF 724	
٥y	841	ے	
Ор	725	-NSDKGYALAEGTRITLSGKNAGFRANGRDYSVIQDLQQLRGIDRDLGGSYVLGN- 778	
οy	889	SLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGT 928	
g	779	83	
y q	929	ABINITGGVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSL 974	
3	0.00	0 0	
Qy Dp	975	NITDSNNDABIQIGGNISQKEGNUTISSNXINITKQITIKKGIDGEDSSSD 10.25 : ::	
>	1026	ATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTVTF 1082	
2 B	932	:     : :   :   ::   :   ::   :   :	
δ	1083	NNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKDIT 1136	
Dp	968	:     :      :      :   : :      :   :	
Οy	1137	SLKTVNITASEKVTTTAGSTINATNGKASITIKTGDISGTI 1177	
Dp	1022	:	
Qy	1178		
QQ	1075	_	
δy	1218		
qq	1133	INGSVINGSA-SGEVTDGSGKTLGGLIGSNLGGNHSNLKASGWVNAGANSDVGGLIGHNR 1191	
Qy	1253	-GNTLTTEAGSSITSTKGQVDLLAQNGSIAGSINAANVT-LNTTGTLTTVAG 1302	
QQ	1192		
δy	1303		
οp	1247	SDLRGSLMLASSHGIVNDKTSHNLGGLVGRGENTSIRSAKASGAVSGGAGIRAGGLV 1303	

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Till—

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

X MEDLINE-21470413; PubMed-11586360;

A BEDLINE-21470413; PubMed-11586360;

A Perthill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Perthill J., Wren B.W., Thomson N.R., Broken C., Mungall K.L., A Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Chillingworth T., Cronin A., Bovies R.M., Davis P., Dougan G., Chillingworth T., Holroyd S., Jagels K., Karlyshev A.V., Lether S., Moule S., Oyston P.C.E., Quail M., Rutherford K., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Nature 413:523-527(2001).

R EMBL, AA14146; CAC89847.1; -

R InterPro: IPR004899; Pertact_sup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1032 LDL----LVNGTAITSGTQCQCAIQQGGSTVA-----NAIHNYGLASSNSNGDSGLXVN 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1138 NRYEGTTTVTAGELILGANGAFGQTSLLDIASGASANINGYSQTVGAVTNVGTVTLGSGG 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1198 V--LTSGLLTNGGILDLTGGALNLTAGGASTVAGGLTGAGTLNI-------N 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1241 GNLSVSAANSGLSGQTHIADVASVTLTDTGTLGTSAVEVLGTLNLNGANAAMTN---- 1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1296 -- VLSGDG-TINTNAAVTLSGNNSFSGAHOIGTDGELTVGQASNLGASSATVNLGTLTSH 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 VTSNQISQLKGILDSNGQVFLINPNGITIGKDAIIN------T 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 NGFTASTLDISNENIKARNFTFEQTK-------DKALAEIVNHGLITVGKDG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 SVNLIGGKVKNEGVISVNGGSISLLAGQKITISDIINPTITYSIAAPENEAVNLGDIFAK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 GGNINVRAATIRNQGKLS-AD--SVSKDKSGNIVLSAKE--GEAEIGGVISAONQOAKGG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     325 KLMITGDKVTLKTGAVIDLSGKE--GGETYLGGDER---GEGK----- 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---NGI--QLAKKTSLEKGSTINVSG-----KEKGGFAIVWGDIALI------DG 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 SGLQGMDVVHGTA-TMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENNNSAVFNR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

8.1%; Score 602; DB 16; Length 3705;
Best Local Similarity 21.7%; Pred. No. 7.8e-12;
Matches 413; Conservative 260; Mismatches 695; Indels 534; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 NALVAVSELA--RGCDHSTEKGS---EKPARMKVRHLALKPLSAMLLSLGVTSIPQSVLA 68
                                                                                                                                                                                                                                                                                                                              Yersinia pestis.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                             1304 GSLEGWQALILGASAGGDVTAGYDSYIGGLVGFSTATISGASASGKVG 1351
1341 ------GSVTAATSSSVN--ITGDLNTVNGLNIISKDG 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1656; VACCYTOTOXIN.
Hypothetical protein; Complete proteome.
SEQUENCE 3705 AA; 370478 MW; 8D36DAB27F85F284 CRC64;
                                                                                                                                                                                Q81HA1.
Q82HA1.
Q82HA1.
01-MAR-2002 (TrEMBLEAL 20, Created)
01-MAR-2002 (TrEMBLEAL 20, Last sequence update)
01-UNY-2002 (TrEMBLEAL 21, Last annotation update)
Putative autotransporter protein.
                                                                                                                                                                PRT; 3705 AA.
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=632;
                                                                                                                                                                   Q8ZHA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363
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3	TOOT	LILINGVSESTANVLSGVAGSTVDIIGGADTALTANNSGFLGQYALAGNSKLTVASTN	1409
δλ	402		442
g	1410	NLCASSSVALAGAGDTLSLSGFNGTFGNSVTGSGVLQVTDDAEVTLTSSNGVSNAVTDI	1469
δ d	443		487
3 8	7	ADAL ENLUDIALF NHVETGNGLLNVAKNDASTA	1523
<u> </u>	1524	LONI LANAMINALTAD KKLITANSZINI GSNSHLILHSKGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	536
3 :	1064	4	1581
S S	1582	TITSNCCHLITITSSCGNUVOVHKNITLDQGFLNITAASVAFEGGNNKARDA   11   1   1   1   1   1   1   1   1	585
á	586	ANAKIVAOGTVITIGEGKDFRANNVSINGFG-	
o Q	1637	::     :	010 1696
ογ	617		668
Q	1691	LLANGANALLLATESGLTANRVLNAELFGVGGLVVDAQNGALTLANGNNRYEGTTTVTAG	1756
δ	699		708
qq	1757	ELILGANGAFGQTSLLNIASGASANINGYRQTVGAVTNSGAVTLGNGGVLTSGLLTNGG	1816
λo	709	SFNLKEGAKVNFKLKPNENMNTSKPLPIRFLANITATG	746
Q D	1817		1876
y d	747	GGSVPFDIYANHSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFS  ::	806
}		otorvevedelene-ngrnrrrinvedgggvininarvilggnnsfsg	1926
g g	807 1927	LRQTKDDFYDGYARNAINSTYNISILGGNVTLGGQNSSSSITCN-ITIEKA     :	856 1986
ά	857		916
g	1987		2032
λά	917		962
q	2033		2086
à	963		1013
q	2087	:: : : : : : :   :   :   :   :   :	2146
ά	1014		1051
ą	2147	GVVTVTDLALNSGTISITGAG	2206
λ̈	1052	TFNNVKDSKIS	1091
q	2207	IDADNVTGNANDLELMINGTTISAGQGVQSTVQ	2266
ζ	1092	ITAKNVEVN	1132
g	2267	QGGYTVANATHNYGWTSNGGSGLYVNYTLSALELLADGANALLLATESGLTANRELN ;	2323
⋩	1133	KDITSLKTVNITASEKVTTTAGSTINATNGKASITTKTGDISGTIS	1178
ą	2324		2382
λ	1179		1218
ð	2383	A'INGYRQTVGAVTNTGTVTLGNGGELTSTDTLINTGMINVTDGILNLENGGASSISGGL :	2442

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1219 SGNTVNVTANAGDLTV----GNGAEINATEGAATLTATGNTL--TTEAGSSITSTKGQV 1271
                         1272 DLLAQNGSIA-----GSIN-AANVTLN------TTGTLTTVAGSDIKATSGT- 1311
                                                                                                        1312 -----LVINAKDAK----LNGDA-----SGDSTEVNAVNA-----SGSGSVT 1344
                                                                                                                                                                                               2561 NLGTLTSHLILNGVSESIANVLSGVAGSTVDIIGGADTALTANNSGFLGQYALAGNSKLT 2620
                                                                                                                                                                                                                                       1345 AAT-----SSSVNI--TGDLNTVNGLN-------IISKDG-RNT 1373
                                                                                                                                                                                                                                                                  1374 VRLRGKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLGVSAVRFVEPNNT 1433
                                                                                                                                                                                                                                                                                                                                                          2681 VIIDIADATLNL--DDIALFNHALTGNGLLNVAKNDASTAFDFGATVGGAFTGTVNLNNS 2738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1032 LDL----LVNGTAITSGTQGVQSAIQQGGSTVA-----NAIHNYGLASSNSNGDSGLYVN 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  972 SGVVTVTDLALNSGTVNITGSGSWDNTDPLATNVSILEQDRAGSTLELINATNVTGDIDA 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.0%; Score 594; DB 2; Length 3705;
Best Local Similarity 21.5%; Pred. No. 1.4e-11;
Matches 409; Conservative 262; Mismatches 695; Indels 538; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 VTSNQISQLKGILDSNGQVFLINPNGITIGKDAIIN---------T 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       165 NGFTASTLDISNENIKARNFTFEQTK-------DKALAEIVNHGLITVGKDG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 SGLQGMDVVHGTA-TMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQFLQENNNSAVFNR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 SVNLIGGKVKNEGVISVNGGSISLLAGQKITISDIINPTITYSIAAPENEAVNLGDIFAK 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 NALVAVSELA--RGCDHSTEKGS---EKPARMKVRHLALKPLSAMLLSLGVŢSIPQSVLA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Henderson I.R., Nataro J.D., Cappello R., Stein C.;
Subultionary origins of the autotransporter proteins.";
Submitted (APR-2000) to the EMBL/GenBank/DOBJ databases.
EMBL, AJZ77631; CAC14227.1; -.
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PRINTS; PR01656; VACCYTOTOXIN.
SEQUENCE 3705 AA; 370756 MW; 714FDF16455968C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               1434 ITVNTQNEFTTRPSSQVIISEGKACFSSGNGARVCTNVADDG 1475
                                                                                                                                                                                                                                                                                                                                                                                                                        2739 TFDLSGNNTTVLAQATLKLSSGNLT-SVGNGVQNIGTLAMNG 2779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 3705 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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1240	324 1295	362 1352	401	442 1469	487 1523	536	585 1636	616 1696	668	708	746 1876	806 1926	856 1986	916 2032	966 2084	1011	1049	1089
1198 VLTSGLLTNGGILDLTGGALNLTXGGASTVAGGLTGAGTLNIN	270 GGNINVRAATIRNQGKLS-ADSVSKDKSGNIVLSAKEGEAEIGGVISAQNQQAKGG :	325 KLMITGDKVTLKTGAVIDLSGKEGGETVLGGDERGEGK	363NGIQLAKKTSLEKGSTINVSGKEKGGFALVWGDIALIDG	402 NINAQGSGDIAKTGGFVETSGHDLFIKDNAIVDAKEWLLDF	443 DNVSINAED-PLFNNTGINDEFPTGTGEASDFKKNSELKTTLTNTT:::	488 ISNYLKNAWTMNITASRKLTVNSSINIGSNSHLILHSKGQRGGGVQIDG	537DITSKGGNLTIY-SGGWVDVHKNITLDQGFLNITAASVAFEGGNNKARDA				709SFNLKEGAKVNFKLKPNENMNTSKPLPIRFLANITATG	747 GGSVFFDIYANHSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFS 	807 LRQTKDDFYDGYARNAINSTYNISILGGNVTLGGQNSSSSITGN-ITIEKA	857 ANVTLEANNAPNOQNIRDRVIKLGSLLVNGSLSLTGENADIKGNLTISESATFKGKTRDT	917 LNITGNFTNNGTAEINITQGVVKLGNVTNDGDLNIT-THAKRNQRSIIGGD 1:::	967IINKKGSLNITDSNNDAEIQIGGNISQKEGNLTISSDKINITKQI	1012 TIKKGIDGEDSSSDATSNANLTIKTKELKLTE-DLSISG	1050 FNKAEITAKDGRDLTIGNSNDGNSGAEAKTVTFNNVKDSK   : :    : :    :
Q	Qy Dp	Oy.	Qy	Qy Dp	Qy Db	Oy Db	. QQ	yo 4	yo da	Oy Dp	Oy Db	O <sub>Y</sub>	Qy	Qy	Qy Db	δy	Qy Db	Oy

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83;
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                                                                                                                                                                                                                                                               1270 QVDLLAQNGSIA-----GSIN-AANVTLN------TTGTLTTVAGSDIKATSG 1310
                                                                                                                                                                                                                                                                                                                                           1343 VTAAT-----SSSVNI--TGDLNTVNGLN------------IISKDG-R 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1372 NTVRLRGKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLGVSAVRFVEPN 1431
                                                                                                                                                                                                         2382 -SANINGYRQTVGAVTNTGTVTLGNGGELTSTDTLINTGMINVTDGILNLENGGASSISG 2440
                                                                                                                                                                                                                                                                                                                                                                                      1311 T------LVINAKDAK----LNGDA-----SGDSTEVNAVNA-----SGSGS 1342
                                                       1131 VNKDITSLKTVNITASE-------KVTTTAGSTINATNGKASITTKTGDISGT 1176
                                                                                                                                                                      1177 ISGNTVSVSATVDLTTKSGSKIEAKSGE-------ANVT-----SATGTIGG 1216
                                                                                                                                                                                                                                            1217 TISGNTVNVTANAGDLTV----GNGAEINATEGAATLTATGNTL--TTEAGSSITSTKG 1269
2205 AGNWENEHPVTPPNVSLLEQDRGDILLQLIDADNVTGNANDLELMINGTTISAGQGVQST 2264
                                1090 ISADGHNVTLNSKVKTSSSNGGR------ESNSD------NDTGLTITAKNVE 1130
                                                                                                                                     2322 LNAELSGVGGLVVDAQNGALTLANGNNRYEGTTTVTAGELILGANGAFGQTSLLNIASGA 2381
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MEDIALINE-99933.
MEDIALINE-99933.
Ward C.K., Lumbley S.R., Latimer J.L., Cope L.D., Hansen E.J.;
"Haemophilus ducreyi secretes a filamentous hemagglutinin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 11, Last annotation update)
10-JUN-2002 (TrEMBLrel. 2).
LSPA2.
Heamophilus ducrey1.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Heamophilus.
NCBI_PA3);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF05766; AAC79761.1;
InterPro; IPR0001951; Verhae_surfAg.
InterPro; IPR000130; Zn_WTpeptdse.
Pfam; PF01543; YorHae_surfAg; 1.
SMART; SM00235; ZnMc; 1. 542595 MW; 5779201455CA69A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1432 NTITVNTQNEFTTRPSSQVIISEGKACFSSGNGARVCTNVADDG 1475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 180:6013-6022(1998).
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3 NKRYKLIFSKVKNCLVPVAENIKSASGNSGSSSNSKIAEDQEEEPDSLACSLSPLSSSIH 62	45 LALRPLSAMILSLGVTSIP-GSVLASGLQG-MDVVHGTATMQVD 86	12	NGAEANVELEE NSAVE		23 SEVVEPHIKQLNVQRGKVIIGKDGVATURGGGGV 278	225 SYNGGSISLLAGQKITISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRA 277	MITGDKVTLKT	DERGEGKNGIQLAKKTSLEKGSTINVSG 38	348DKGAGVNHQGVIFAEDDINILTDDGNSRLNKVYADYVRVVG 388	44	:  ::  :             ::   ENATVSANNILSFRUTNDFKLNNLSKVSARAADLQSGNLNLDRASVLAHKLTLNISNDVSL 49	489 SNYLK-NAWTMNITASRKLTYNSSINIGSNSHLILHSKGORGGV 532 	QIDGDITSKGGNLTIYSGGWVDVHKNITLDOGFLNITAAS ::	VAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTG	KGLNITSSVNNITHNISELAANNLSLAASHNYTLNNKSKLSAQKADIKAVNLTLNDTTELTA 67	:    :	SALNLETGANFTEIKYISSNSKGLTTQYRSSAGVVFNGVNGNMSFNLKE 71 :		GFFTNSGNLTTVKTLDVGDIQNFTNKGNLTVGEDLHIKSKTKITNDGKLISIKNL 83	NISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARN 82    :  :  :  :  :  :    NISSEADFINNGTLLGIEALKIATKGNFTNFRRATIASNSTIDTSNAFOFFFFNNGTL	DINGS AND COLUMN TO CARREST CONTRACTOR COLUMN TO CARREST CONTRACTOR COLUMN TO CARREST COLUMN TO CARRES	12 NITESTALELEGANYTIGGONSSSSITGNITTERANNYTLEANNAPHOQNIRDRVIKLGS 881 1   1:1		
qq	Oy 4:	Oy 87		Db 173 Ov 172		Qy 225 Db 279	Oy 278 Db 313	Фу 338	Db 348	Oy 384 Db 389	Db 437	Oy 489 Db 497	Qy 533 Db 557	Oy 573			Oy 666 Ob 725	Qy 715	Db 784	Oy 771 Ob 839	922		Qy 882 Db 938	
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971 KOGNITNKNLIASROOLNLTAVADNITNDSNISNKIAVLHSLGNISLNSKDOVYNLGEIY 1030
                                                                                        987 IGGNISQKEGNLTISSDKINITKQITIKK-------GIDGEDSSSDATSNAN 1031
                                                                                                                                   1031 AGNNISVKAHQL---KNDVKLMGDITTKTKEGQASYKLYQASNGGHFGNDGSS-GYSEGD 1086
                                                                                                                                                                                                           1032 LTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTVTFNNVKDSKIS 1091
                                                                                                                                                                                                                                                                       1092 ADGHNYTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKDITSLKTVNITASEKVTT 1151
                                                                                                                                                                                                                                                                                                                1129 NRG---TINVKNKLSYDSDVSFENNMOSOKVDLYTKIFEAKSDIE--LTFKTNGTHPVYL 1183
                                                                                                                                                                                                                                                                                                                                                              1152 TAGSTINATNGKASITTKTGDISGTISGNTVSVSATVDLTT-KSGSKIEAKSGEANVTSA 1210
                                                                                                                                                                                                                                                                                                                                                                                                      1184 NFKSNNNEKKYRNSENTKNFKSIGDLINEALSDSAPEAIEAYYSGS----SSNYINPVSY 1239
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1211 TCTIGGTISGNTVNVTANAGDLTVGNG--AEINATEGAATLTATGNTLTTEAGSSITSTK 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1240 LAALGNANNSSNPHYLNTALKHILGNGWQDDLKKQENIKVLKQKWEDFKKDKGAS---- 1294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1269 GQVDLLAQNGSIAGSINAANVTLNTGTLTTVAGSDIKATSGTLVINAKDAKLN-GDASG 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1295 KMLDLYPNTDKEKAKI-FAGIIRNGNDTISDVESEDFRKKYSKFQ-NGEWAKNDTGTDSY 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1328 DSTEVN----AVNASGSGSVTAATSSSVNITGDLNTVNGLNIISKDGRNTVRLRGK--E 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             939 KLGNVTNDG-----DLNITTHAKR--NQRSIIGG-DIINKKGSLNITDSN---NDAEIQ 986
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Best Local Similarity 22.4%; Pred. No. 1.2e-10;
Matches 326; Conservative 187; Mismatches 546; Indels 396; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1381 IEVKYIQPGVASVEEVIEAKRVLEKVKD--LSDEERETLAKLGVSAVRFVEPNN 1432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid megaplasmid.
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
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EMBL; AL646085; CAD18690.1; -
InterPro; IPRO00566; Lipocln_cytrABP.

PROSTIE: 9870213; LIPOCALIN; UNKNOWN_1.

Plasmid; Complete proteome.

SEQUENCE 2737 As: 268490 MW; 12F383C02C101D0C CRC64;
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UN-2002 (TrEMBLrel. 21, Last annotation update)
Probable hemagglutinin-related protein.
RSP1539 OR RS05770.
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SEQUENCE FROM N.A.
STRAIN=GMI1000;
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δy	82 TMQ	EMVQFLQENNNSAVFNRVTSNQISQLKG	138
Dp	155 SLT	LTOVIGTEPIRINGTVE	212
Oy Db	139 ILD:	ILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIKARNFTFEOTKDKALAEIV ::	198 270
		OKITISDII	245
qq	271 NSG	ď	319
οy	246 NPT		288
qq	320 GNO	GNOOVAPVATGTGRAGSDWQVSGAGANAAANSASAQNGLAIDATAFGAMTAGQIKLISTA	379
	o.	KLMITGDKVTLKTGAVID	342
Dp	380 OGD	LAANTSNVNIDANGDVSVGNVYGQQTAGITTTGSVSTSGAVRAQQD	435
Qy	343 LSG	GEGKNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWGDIALID	400
qq	436 VTI	AGSGDLAAVHGLSVSAGNSANLG	487
οy	401 GNI	AQGSGDIAKTGGFVETSGHDLFIKDNAIVDAKEWLLDFDN	444
qq	488 GNL	GNLNAASIAVTAQGKDGTGDITLGGKVASPGGIALNAARDTTIAGQLTGGSG	539
δy	445 VSI	VSINAEDPLFNNTGINDEFPTGTGEASDPKKNSELKTTLTNTISNYLKNAWTMNITASR	504
Dp	540 VSV	GRNLSVSGAIGSVGDLNLAAAAGSVSTTGAV	585
Qγ	505 KLT	KLTVNSSINIGSNSHLILHSKGQRGGVQIDGDITSKGGNLTIYSGGWVDVHKNITLDQ-	563
Dp	286 GQD	NGHVAIQANAGSIT	635
Qy	564	-GFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTGKGL	619
qq	636 TQT	TQTGGNLTVTAGNTVGGAGNLTASKAIDVQAGGSVDVSGNVSANRIAMQAAGR	688
Οy	620 NII	SSVNNL	629
QQ	689	DGVGDIRLGGNVGAPGTITLN-AARDTTIAGSVVSDSDLN	727
Qy	680 KYI	ISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFL	739
Dβ	728	LATQRNLSVGGVVGSTKGNVSLTARTGA	755
Qy	740 ANI	ř.	199
οqα	756	:1 : : : : : : : : : : : : : : : : : :	791
Qy	800 ATN	ATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGGGNSSSSITGNITIEKAANV	859
qq	792	STAGOIGS	816
δy	860 TLE	ŏ	918
q	817 TIC	TIGGQVGSGADANLQAGSNVTVNGALTSTG-NASVLAGQSIAT	857
οy	919 ITC	TOGVVK	211
QQ	858 LAC	LAGDVAAGGNATLDASQTITGPGNLSAAQTAKVTGGSIDLGGQVKGKQVALTAN	911
QY	978 DSI	DKIN	1023
qq	912 GSC	GSGNLGDVRLGGAVG-APGSVTISATRDATLGSNAIAGGDLIATAGRNLTVNGAA	965
ογ	1024 SDAT:	ATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAK	107
QQ	966 AS	ASVNGNVNLTAQAGQLASTGSIQANQGDVNATAGQGLNVGGSVYAGRNAGLVAQGGN	1022

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61;
1079 -TVTFNNVKDSKIS-ADGHNVTLNSKVKT-----SSSN------GGR------ 1112
                                           1023 ATVSGNLTSLGKASIGSGGNTTLSGQLKTGGDLQASAANALSVAQLNYVGGNAILRGTDI 1082
                                                                                                                                                               1155 STINATNGKAS-ITTKTGDI--SGTISGNTVSVSATVDLTTKSGSKIEAKSGEANVTSAT 1211
                                                                                                                                                                                                         1142 MVTNAGMLAANQLTVSATDLVNRGTVGGQAVKLNTTGNLDNAGGLVVGSQTLDVTAGALT 1201
                                                                                                                                                                                                                                               1212 GTIGGTISGN-----ATE 1244
                                                                                                                                                                                                                                                                                           1202 SNRGGTFFGGDLAGKSPTTGNLTFTVNGGAGSFNNAGGQLLAGNNLTLNTPNQAFDPSAA 1261
                                                                                                                                                                                                                                                                                                                                  1245 GAATLTATGNTLTTEAGSSITSTKGQVDLLAQNGSIAGSINAA-------NVTL 1291
                                                                                                                                                                                                                                                                                                                                                          1292 NTTGTLTT----VAGSDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAAT 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROW N.A.
STRAIN-ATCC 15692 / PAO1;
STRAIN-EATCC 15602 / PAO1
STRAIN-EATCC 15602 / PAO1
HCKPA N.J. Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Hackey N.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M., Broker R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Santh K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulesen I.T., Relzer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1113 -----ESNSDNDT-----GLTITAKNVEVNK----DITSLKTVNITASEKVTTTAG 1154
                                                                                                                           1083 AVGSAAGQSNAVQGTLDAVASRGLTL-AGNSNANALNLGGATIVNQGSTLATQRATVSGG 1141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 GVTSI-PQSVLASGLQGMDVVHGTATMQV---DGNKTIIRNSVDAII-NWKQFNIDQNEM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.5%; Score 553.5; DB 16; Length 1018; Best Local Similarity 22.6%; Pred. No. 7.4e-11; Matches 301; Conservative 181; Mismatches 453; Indels 399; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNKIYRLKFSKRLNALVAVSELARGCDHSTEKGSE---KPARMKVRHLALKPLSAMLLSL 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNKCYAL-----AIASVLALL 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opportunistic pathogen.";
Nature 406:959-964(2000).
BMBL; ARG04824; A-CCOMPLete proteome.
COMPLETE PROTECTION NA: 100433 MW; F373734D77FFA94D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-0CT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1018 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1348 SSSVNITGDLNTVNG 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1373 GSNYDNOGGKTQANG 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probable adhesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=287;
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QQ	101	1 VIFNQPSSSSIALNRVIGTKASDIQGRIDANGQVFLVNPNGVLFGRGAQVNVGGLVASTL 160	
οy	173	DISNENIKARNFTFEQTKDKAL	
QQ	161	DITDAE	
δγ	228		
рp	216		
δ	280	IRNQGKLSADSVSKDKSGNIVL-SAKEGEAEIGGVISAQNQQAKGGKLMITGDKVT 334	
g ,	276		
δ	335	LKTGAVIDLSGKEGGETYLGGDERGEGKNGI	
qq	335	VALGTQVNTLASNGLNGTWKIAADKIDVRPSAVSDGVTVHADTLSRN 381	
ΟY	393	MGD	
qq	382	LASTNIELVSTKGDLDLDGSVNWASGNRL	
ογ	452	PLFNNTGINDE	
QQ	411	GLGSA	
οy	512	INI	
Dp	441		
٥y	565	FINITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTGKGLN 620	
οp	494	LAQLQAINKNLDGLYVLGGNILGGSYYCTALQSIGGPAG 532	
οy	621	IISSVNNLTHNLSGTINISGNITINQTTRKNTSYWOTSHDSHWNVSALNLETGANFTFIK 680	
QQ	533		
οy	681	YISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFLA 740	
рp	558		
δy	741	NITATGGSVFFDI 	
QQ	594	GINSGRIANVSASGVSVVGSRLRSNALGGLVGRNISGQI 632	
ý á	801	TNSNESLRQTKDDFYDGYARNAINSTYNISILGGNVTLGGGNSSSITGNITIEKA-ANV	
2 .	650		
o P O	960	TLEANNAPNQONIRDRVIKLGSLLVNGSLSLTGENADIKGNLTISESATFKGKTRDT 916	
Qγ	917	LNITGNFTNNGTAEINITQGVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSL 974	
g G	718	LINVGGLVGYNMFGHVSDSSASGQVEAGGAGNTGGLVGLSSGGEIFRSQASGSVYSKGG 775	
οy	975	NITDSNNDAEIQIGGNISQKEGNLTISSDKINITKQITIKKGIDGEDSSSDATSNANL 1032	
QQ	776	::    :   :   : :   ::    : :   : : : :	
Qy Dp	1033	TIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTVTFNNVKDSKISA 1092  :	
٥ م	1093	DGHNVTLNSKVKTSGSNGGBESNSDHDGI #I## XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	
- qq	860	GGFNSLVGGIVGHNGG	
λά	1153	AGSTINATNGKASITTKTGDISGTISGNTVSVSATVDLTTKSGSKIEAKSGEANVTSATG 1212	
g	890	ASASVGGLVGSNAGSLLSARSSTVNGSGRSRIGGIVGENOIOG 933	

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82;
1213 TIGGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEAGS-SITSTKGQV 1271
                          : || ||| |: | ; | ; | 1010 GI---GVGIVNGSSGTLTFGAGSSIAGTSSNAFSISNSTPNVTYNGTISGTSAASAVKIS 1066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.4%; Score 548; DB 16; Length 3930;
Best Local Similarity 21.9%; Pred. No. 4.8e-10;
Matches 366; Conservative 227; Mismatches 641; Indels 441; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 SLGVTSIPQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAIINWKQFNIDQNEMVQF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                861 SLGGVPI-----NITGDNVAHDVAISDPGGAATLINSGSGAVVI----AANGNSLLDF 909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 LQENNNSAVFNRVTSNQISQLKGILDSN------GQVFLINPN-----GI-TI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             910 NISGGSDAGINATSINGLT-IQGVIVSNVDIGLFLGSVTGTVSVDNLNVONASQTGIELL 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 GKDAIINTNGFTASTLDISNENIKARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGG 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 KVKNEGVISVNG-----GSISLLAGQKITISDIIN--PTITYSIAAPENEAVNLGDIF 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 -AKGGNINVRAATIRNQGKLSADSVSKDKSGNI-VLSAKEGEAEIGGVISAQNQQAKGGK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 LMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGEGKNGIQLAKKTSLEKGSTINVSGKE 385
                                                                                                                                                                                                                                                                                                                                         Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9ACD1ACA185BF712 CRC64;
                                                                                                                                                                                                                                                  01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein ml14444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
EMBL; AP003004; BAB511000.1;
InterPro; IPR0001425; Bac_rhodopsin.
InterPro; IPR000734; Lipase.
InterPro; IPR00380; Ppantne_attach.
INTERPROSITE; PS00127; BACTERIAL_OPSIN_ET; UNKNOWN_1.
PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
PROSITE; PS00121; PHOSPHOPANTETHEINE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Complete proteome.
SEQUENCE 3930 AA; 380662 MW; 9ACDIAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-MAFF303099;
MEDLINE=21082930; Pubmed=11214968;
                                                                            1272 DLLAQN--GSIAGS 1283
                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                   973 DFKPQSHYGQIYGA 986
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SEQUENCE FROM N.A.
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Qy Dp	386	KGGFAIVWGDIALIDGNINAQGSG-DIAKT-GGFVETSGHDLF-IKDNAIVDAKEWLLDF 442 ::: :  :		Ω
QY	443	DNVSINAEDPLFNNTGINDEFPTGTGEASDPKKNSELKTTLTNTTISNYLKNAWTMNITA 502    :		0 0
Qy Db	503 SRKLTVNSSINIGSNSHLIL : ::: : : 1246AGADVSLINNT	SRKLIVNSSINIGSNSHLILHSKQQRGGQQIDGDITSKG-GNLTIYSGGWVDVHKNITL 561 ::::: :::::::::::::::::::::::::::::::		Q Ω
Oy Op	562 DQGFL      1288 D	DQGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTGKGLNI 621 		0 0
Qy Db	622	KNTSYWQTSHDSHWNVSALNLET :   :   : : : : AANAAGI NFSGTNADVLFGTTNVTMGA		K OH
O.y	673	GANFTFIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFULKEGAKVNFKLKPN 725        :  :       :    :    :    :	~	4 D D D
Oy Db	726	ENMNTSKPLPIRFLANITATGGGSVFFDIYANHS-GRGAELKMSEINISNGANFTLNSHV 784  :		
Qy Dp	785	RGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGUVTLGGON 842		0 22 22 22
Oy Dp	843	SSSSITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLVNGSL- 888		***
Qy Dp	1607			***
Qy Db	923	FTNNGTAEINITQGVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSL-N 975		K U K W
oy Db	976	ITDSNNDAEIQIGG-NISQKEGNLTISSDKINITKQITIKKGIDGEDSSSDAT 1027    :  :  :  :  :  :  :  :  :  :  :  :  :		
Qy Db	1028	SNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTVTFNN 1084		Ø D
ç O	1085	VKDSKISADGHNVTLNSKVKTSSNGGRESNSDNDTGLTIT 1125		0 0
Qy Dp	1126	AKNVEVNKDITSLKTVNITASEKVTTTAGSTINATNGKASITTKTG 1171 		0 0
Qy Db	1172	DISCTISGNTVSVSATVDLTTKSGSKIEAKSGEANVTSATGTIGG 1216 :   :   :		Ø 11
7 2 2	1217	-TISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNT 1255   :		о п
Oy Dp	1256	1256 LTTEAGSSITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVAGSDIK 1306 ::     :		3 4
ΟŸ	1307	SDSTEVNAVNASGSGSVTAATS 1348		G

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1349 ----SVONITGDLNTVNGLNII-----SKDG--RNTVRLRGKEIE- 1382
                                                                                                                                                                                                   2179 QVIHATDTLPTSGDYNFNDVNFSGDTSNLSAVRVYYVTAGGTGDGSLANPGSYLGAQAST 2238
                                                                                                                                                                                                                                                                                                                                  1383 ---VKYIQPGVASVEEVIEAKRVLEKVKD-----LSDEERETLAKLGV-----SAV 1425
                                                                                                                                                                                                                                                                                                                                                                                                                              2239 ANVVVLIDKNVNGAQETIDLSGTTFNLDDGQVLLAFKSGDAAVDVSQLGVDTSGGASAAF 2298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.3%; Score 543; DB 16; Length 3165;
Best Local Similarity 22.5%; Pred. No. 5.6e-10;
Matches 372; Conservative 222; Mismatches 535; Indels 524; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 ASGLQGMDVVHGTATMQVDGNKTII----RNSVDAIINWKQFNIDQNEMVQFLQENNNSA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 396 AVGLYSADPTKFNNTFKIESGKTLDVELGKNSTFGLLNGNN-TVTNSPLLSKYLNNNTSD 454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                455 KINIVSFGEGASLFYATSKAKAILDEDYKVTNGDAISTAVLVANNGANVEIASGKKLETN 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STARIN-ATCC 25586;
MEDLINE-21886394; Pubmed-11889109;
Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
Rapatral V., Anderson I., Ivanova N., Gardner W., Grechkin G., Zhu L.,
Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
Fonstein M., Kyrpides N., Overbeek R.;
"Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";
"Genome sequence and analysis of the oral bacterium Fusobacterium
Complete proteome.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2299 HFTTIQNTPIISAPGGIDTLRPVLQSNNATSVINFATSGTGTFTGGIENLIVSNV 2353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1426 RFVEPNNTITVNTQNEF-TTRP-----SSQVI--ISEGKACFSSGNGARVCTNV 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Fusobacterium outer membrane protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 3165 AA.
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Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
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Best Local Similarity
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QΩ	737	:   :	6
οy	439	LLDFDNVSINAEDPLFNNTGINDEFPTGTGEASDPKKNSELKTTLTNTTISNYLKNAWTM 49	8
QQ	770	78 VGISVDGSSTGEND 78	Э
Qy Dp	784	NITASRKLTVNSSINIGSNSHLILHSKGGRGGVQIDGDITSKGGNLIXSG 550	
oy Op	551 838	GW IF	0 8
ç, q	611	SLNGTCKGLNIISSVNNLTHNLSGTINISGNITINQTTRKNTSYWQTSHDSHWNVSA-  :	
δy	668	LNLETGANFTFIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEG	n 10
Вb	926	TINSCKIEVKNEGSAGVLAEKYKVTNTGSGINGIIVSAKKSAGIIGKLGSEI	7
95 Pp	716	AKVNFKLKPNENMNTSKPLPIRFLANITATGGGSVFFDIYANHS 759	9
οy	760	GRGABLKMSEINISNGANFTLNSHVRGDDAFKINKD-LTINATNSNFSLR	, 
QQ	1025	MYGEANSQLTNEGNIT-GINKEYIVGMAGDSSTVTNKNIITLNGKKATGIFGKNSSTLLN 108:	83
οy	808	OT	0
QQ	1084	ETTGKIPTKEEESVGMYSSSSLKATNKGTITTEKKTSAGMLGDKANIENDSSIPTKEEMS 114	43
Oy Op	841	ONSSSITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLVNGSLSLT 891 :  :      :    :    :    :	184
οy	892	NITGNFTNNGTAEINITQGVVKLGNVTNDGDL 94	6
g	1185	GLN-ETTGTITVSEETSAGMLGKVKSAVTASTAKL-SLTNKKDI 1220	92
oy Ob	950	NITTHAKRNORSIIGGDIINKKGSLNITDSNNDAEIQIGG 989	O O
3 2	1 0	WINDOCKEL WINDERSTANDEN PRENTETINDESSATINDEN TO THE TRANSPORT TO THE TRANSPORT OF THE TRANS	o :
g g	990	NISQKEGNLTISSDKINITKQITIKKGIDGEDSSSDATSNANLTIKTKELKL 104:   :	41 46
γά	1042	TEDLSISGFNKA-EITAKDGSDLTIGNSND 1070	0.0
g G	1347	GEDSGTVKNNKTISVTAEKGVGIFVRDNGVGKGSGTGENTSTGTITLENKEAVGIFAKNN 1406	90
λά	1071	GNSGAEAKTVTFN	25
q O	1407	GTSDSAKNSGTINLGKADGSTIKESLIGMFAQAEAGKKANVKNTKDINVNTKKS 1460	20
ά	1103	VKISSSNGGRESNSDNDTGLTITAKNVEVNKDITSL 1138	88
g	1461	VGIYAKNDASNITDVDLENTGDININSKESAGVYAPKANISKVGTITLKNSIDSNGS 1517	71
λά	1139	KTVNITASEKVITTAGSIINA1NGKASITTKIGDISGIISGNIVSV 1184	34
අ	1518	XLQ 157	2
λά	1185	122	98
<b>Q</b> .	1576	KNTSKLDYTLQGTGNGIIGLLLKGETNIQSYTKGIKVGNTVAAT 162	63
27	1227	ANAGDLTVGNGAEINATEGAATLTATGNTLTTEAGSSITSTKGQVDLLAQ 127;	9

GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

March 24, 2003, 15:23:05 ; Search time 26 Seconds
 (without alignments)
5461.175 Million cell updates/sec Run on:

US-10-092-880-4

1 MNKIYRLKFSKRLNALVAVS......CFSSGNGARVCTNVADDGQP 1477 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

283224 seqs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Description	high-molecular-wei	high-molecular-wei	probable adhesin h	hypothetical prote	_	$\sim$	hypothetical prote	hemolysin A precur	probable adhesin P	hemagglutinin/hemo	hypothetical prote	filamentous hemagg	hemagglutinin/hemo	probable hemolysin	hemagglutinin/hemo	type tran	ace	190K surface antig	hypothetical prote	probable adhesin Y	hemopexin-heme com	surface protein XF	hemolysin A - Edwa	hypothetical prote	_	190-KDa cell surfa		hypothetical prote	
SUMMARIES	ID	B43855	A43855	AF0394	F83068	A83080	AD0123	T31105	A35140	H83135	B99789	E85649	T31102	B81192	AC0304	G81044	C48399	B71704	A41477	B81989	AE0074	S54699	D82671	T43072	AG2560	875138	A97859	F90696	AE1852	
	DB							7																						
	Length	1477	1536	1910	2154	1417	3705	4919	1577	1018	1268	1270	4152	1975	2535	1995	2020	2340	2249	2015	3295	928	2059	1594	1487	1749	2021	5291	1152	
оP	Query	8	9		10.1			8.0																		6.4	6.4	6.4	6.4	•
	Score	7327	4957	876	744.5	636.5	602	593.5	555.5	553.5	531.5	531.5	523.5	520	520	517.5	517.5	512.5	511	508	504	486.5	485	480	477.5	475.5	475.5	^	472.5	
	Result No.	-	7	٣	4	2	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	

High-molecular-weight surface-exposed protein - Haemophilus influenzae high-molecular-weight surface-exposed protein - Haemophilus influenzae high-molecular-weight surface-exposed protein - Haemophilus influenzae (; Species: Haemophilus influenzae (; Species: Haemophilus influenzae (; Species: Haemophilus influenzae)	
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; 0 Gaps 0; Query Match

98.9%; Score 7327; DB 2; Length 1477;

Best Local Similarity 99.2%; Pred. No. 3.2e-291;

Matches 1465; Conservative 3; Mismatches 9; Indels 0;

ŏ QQ

121 NSAVFNRVTSNQISQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180 δλ qq 181 ARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 240 οy

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241 ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 300

òγ

241 ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 300 301 LSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGE 360 g Óγ

qq ò

421 SCHDLFTKDNAIVDAKEWLLDFDNVSINAEDPLFNNTGINDEFPTGTGEASDPKKNSELK 480

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SGHYLSIESNAIVKTKEWLLDPDDVTIEAEDPLRNNTGINDEFPTGTGEASDPKKNSEL	TTLINTTISNYLKNAMTMNITASRKLTVNSSINIGSNSHLILHSKGGRGGGVQIDGDIT 	KGGNLTIYSGGWYDVHKNITLDQGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITI 	EGKDFRANNVSLNGTGKGLNIISSVNNLTHNLSGTINISGNITINQTTRKNTSYWQTSHD 	SHWNVSALNLETGANFTFIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNF 	KLKPNENMNTSKPLPIRFLANITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTL 	NSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGG 	ONSSSSITGNITIEKAANVTLEANNAPNQONIRDBVIKLGSLLVNGSLSLTGENADIKGN 	LTISESATFKGKTRDTLNITGNFTNNGTAEINITGGVVKLGNVTNDGDLNITTHAKRNQR 	SIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKEGNLTISSDKINITKQITIKKGIDGE 	DSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTV 	TFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDFGLTITAKNVEVNKDITSLKT 	VNITASEKVTTTAGSTINATNGKASITTRTGDISGTISGNTVSVSATVDLTTKSGSKIEA 	KSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEA 	GSSITSTKGQVDLLAQNGSIAGSINAANVTLNTGTLTTVAGSDIKATSGTLVINAKDAK 	LNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVNGLNIISKDGRNTVRLRGKE 	IEVKYIQPGVASVEEVIEAKRVLEKVKDI.SDEERETLAKLGVSAVREVEPNNTITVNTQN 	EFTTRPSSQVISEGKACFSSGNGARVCINVADDGQP 1477 
421	481	541	601	661	721	781 781	841	901	961	1021	1081	1141	1201	1261 1261	1321 1321	1381 1381	1441
qq	Oy Dp	Qy Db	oy Db	Qy Db	Oy Dp	Qy Dp	Oy Dp	Qy	ογ Dp	Qy	Oy Db	Ολ Dp	QY Dp	Qy Db	Qy Db	Qy Dp	oy Op

RESULT 2 A43855

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high-molecular-weight surface-exposed protein HWW1 - Haemophilus influenzae C; Species: Haemophilus influenzae C; Species: Haemophilus influenzae C; Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999 C; Accession: A43855 R; Barenkamp, S.J.; Leininger, E. Infect. Immun. 60, 1302-1313, 1992 A; Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable detella pertussis.

A; Reference number: A43855; MUID:92192797; PMID:1548058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NSAVFNRVTSNQ1SQLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKVKNEGVISVNGGSISLLAGQKIT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538 TGDDTRGANLTIXSGGWVDVHKNISLGAQGNINITARQDIAFEKGSNQV-----ITGQ 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 66.9%; Score 4957; DB 2; Length 1536;
Best Local Similarity 67.3%; Pred. No. 1.4e-194;
Matches 1046; Conservative 146; Mismatches 265; Indels 98; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 ISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVSKDKSGNIV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 LSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 GKNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWGDIALIDGNINAQGSGDIAKTGGFVET 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 KTTLINTTISNYLKNAWTMNITASRKLTVNSSINIGSNSHLILHSKGQRGGGVQIDGDIT 539
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. Tue Mar 25 08:37:46 2003

Qy 765 LKMSEINISNGANFTLNSHVRGDDAFKINKDLFINATNSNFSLRQTKDDFYDGYARNAIN	DGYARNAIN 824	One	Query Match
Db 767 INSKYFNVSTGSSLRFKTSGSTKTGFSIEKDLTLNATGGNITLLQVEGTDGMIGKGIV	DGMIGKGIV 824	Mate	ches 421; Cons
QY 825 STYNISILGGNVTLGGQNSSSITCNITIEKAANVTLEANNAPNQQNIRDRVIKLGSLLV :	VIKLGSLLV 884    :: TIKKDVIIN 882	Ογ Dp	2 NKIYRLKFSKR : : :    :  3 SKLYKLIFCRR
QY 885 NGSLSLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGTAEINITGGVVKLGNVT	GVVKLGNVT 944	Oy	62 IPQSVLASGLQ
DD 883 SGNLTAGGNIVNIAGNLTVESNANFKAITNFTFNVGGLFDNKGNSNISIAKGG	GGARFKDID 942	Dβ	63 FPLLVLAHPVL
QY 945 NDGDLNITTHAKRNORSIIGGDIINKKGSLNITDSNNDAEIQIGGNISQKECNLTISSDK   : :   ::	GNLTISSDK 1004 	QY	119 NNNSAVFNRVT :    :  123 GSQSIALNQVQ
Qy 1005 INITKQITIKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFNKAEITAKDGRDLT	TAKDGRDLT 1064               TAKDGSDLT 1062	Qy Dp	179 IKARNFTEGT : :: 183 FLSGDYRLI
Qy 1065 IGNSNDGNSGAEAKTVTFNNVKDSKISADGHNVTLNSKVKTSSSNGGRESNSDNDTGLTI    :  :  :  :  :  :  :  :  :  :  :  :	SDNDTGLTI 1124    :       SDNNAGLTI 1121	O <sub>Y</sub>	237 QKITISD : :: 241 HSVTLNLDHGN
QY 1125 TAKNVEVNKDITSLKTVNITA-SEKVTTTAGSTINATNGKASITTKT	1170 GGIESSSGS 1181	Qy Db	280 IRNOGKLSADS           294 IDNTGILQAKG
Qy 1171GDISGTISGNT	ISGTISGN 1181                 GGTISGGT 1241	Qy	339 AVIDLSGKEGG : 1   1   1   353 SNIKAKGTAGG
QY 1182 VSVSATVDLTTKSGSKIEAKSGEANVTSATGTIGGTISGNTVNVTANAGDLTVGNGAEIN	TVGNGAEIN 1241            TVGNGAEIN 1301	QY	395 DIALIDGNINA             412 DYTGFHGNIRA
QY 1242 ATEGAALLTATGNTLTTEAGSSITSTKGQVDLLAONGSIAGSINAANVTLNTTGTLTTVA 	TTGTLTTVA 1301 	Q.y D.b	446 SINAEDPL :     : 468 TIVSSGAESGV
QY 1302 GSDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVN	ITGDLNTVN 1361          :   ITGDLITIN 1421	Qy Db	502 ASRKLTVNSSI        :   524 TSNSSL
QY 1362 GLNIISKDGRNTVRLRGKEIEVKYIQPGVASVEEVIEAKRVLEKVKDLSDEERETLAKLG	ERETLAKLG 1421              	Oy QD	559 ITLDOGFLNIT          : 567 ITADAGKLNLN
OY 1422 VSAVREVERNNTITVNTQNEFTTRPSSQVIISEGRACFSSGNGARVCTNVADDGO	DDGQ 1476  - - : DNGR 1536	Qy Db	616 GKGLNIIS : :: 614 AR-IGLLGGRY
RESULT 3 AF0394 probable adhesin hmwA [imported] - Yersinia pestis (strain CO92) C; Species: Yersinia pestis C; Species: Yersinia pestis C; Species: Yersinia pestis C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001 C; Accession: AF0394 R; Parkhill, J; Wren, B.W; Thomson, N.R; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; In, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, N. Title: Genome sequence of Yersinia pestis, the causative agent of plague. A; Reference number: AB0001; MUID:21470413; PMID:11586360 A; Accession: AF0394 A; Status: preliminary A; Restudes: DNA A; Restudes: L1910 KRUP> C; Genetics: A; Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN00175 C; Genetics: A; Gene: hmwA	uge 02-Nov-2001 den, M.T.G.; Prentice, M.B. M.; Davis, P.; Dougan, G.; C.; Whitehead, S.; Barrell, lent of plague. 83; GSPDB:GN00175		673 GANFTERKYIS  1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   1   2   1   3   1   4   1   5   1   1   1   1   5   1   1   1   1   1   1   1   2   1   1   1   1   2   1   3   1   4   1   1   1   4   1   6   1   6   1   6   1   7   1   7   1   7   1   8   1   8   1   9   1   1   1   9   1

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11.8%; Score 876; DB 2; Length 1910;
ity 25.5%; Pred. No. 4.1e-28;
servative 235; Mismatches 665; Indels 332; Gaps 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITAASVAFEGGNNKARDAA---NAKIVAQGTVTITGEGKDFRANNVSLNGT 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      )TKDKALAEIVNHGLITVGKDGSVNLIGGKVKNE--GVISVNGGSISLLAG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNLLGVQI-----QGETVAALIQNGGLIQADGGVIQLTAKGKDMLMDTV 293
                                                                                                                                                                                                                                                               RLNALVAVSELARGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVTS 61
                                                                                                                                                                                                                                                                                                                                                                                               REGCLIAVGEFTRSYGRAFSSKGGQAGNNQRRAVGILSRLAMMTGLALGI 62
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146   VPLINPMGITIGKDAIINTNMGFTASTLDISNENIKARNFTEEOTKDKALAEIVNHGLITY 205	
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	
Db 935 LISPETIGE CONTROLLEY AND CONTROLLEY	RESULT 4 F83068 hypothetical protein PA4625 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Species: Dseudomonas aeruginosa C;Species: Dseudomonas aeruginosa C;Accession: F83068 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon A;Reference number: A82950; MuID:20437337; PMID:10984043 A;Residues: preliminary A;Residues: prel

178   NIKARNETFEQTKDRALAEIVNHGLITVGKDGSVNLLGGKVKNEGVISVNGGSISLLAGQ 237   16   16   16   16   16   16   16   1		137 SIKTVNITASSEKUTTURE AND STATEMENT OF STA
	RESULT 5 A83000 hypothetical protein PA4541 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: A83080 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yudan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim., J. Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathchance number: A82950; MUID:20437337; PMID:10984043 A;Residues: preliminary A;Residues: 1-1417 <cspc>A;Cross-references: GB:AE004867; GB:AE004091; NID:g9950769; PIDN:AAG07929.1; GSPDB:GN001 A;Everimental source: strain PA01 C;Genetics: A;Gene: PA4541</cspc>	Query Match         8.6%; Score 636.5; DB 2; Length 1417;           Best Local Similarity 21.9%; Pred. No. 1.6e-18;           Matches 352; Conservative 238; Mismatches 523; Indels 495; Gaps 72;           Qy 1 MNRIYELKFSKELNALVAVSELARGESKPARMYCHLALKFLSAMLLSLGVT 60           1         ::

1074	1217 Qy 363NGIQLAKKTSLEKGSTINV 1132 Db 1353 LILNGVSESIANVLSGVAGSTVDI	1252 QY 402 NINAQGSGDIAKTGGFVE	1302 QY 443 DNVSINAED-PLFNN ::  :       1246 Db 1470 ADATENEDDIALFNHVLTGNGLLN	1340 OY 488 ISNYLKNAWTMNITASRKLTVNSS	Qy 537DITSKGGNLFIY-SGGWVDVH	Qy 586 ANAKIVAQGTVITIG	Oy	Db 1697 LLANGANALLLATESGITANRVLN. P.: Dougan, G.; Oy 669 NLETGANFTFTKYTSSNNKG	S.; Barrell, Db 1	Qy 709SFNLKEGAKVNF :       Db 1817 LDLTGGALNLAAGGSSTVAGGLTGA	Qy 747 GGSVFFDIYANHSGRGAELKMSETI in 1: Db 1877 TGTLGTSAVEVLGTLI	Qy 807 LRQTKDDFYDGYARNAINST)  DD 1927 AHQIGTDGELTVGQASNLGASSATY	33	27 917 LNITGNFINNGTAEINIT-QGVVKI 127   1::	QY 963 IGGD-IINKKGSLNITDSNNDAEIG 164   :     :   :   Db 2087 ALFDHVLTGNGTLNVAKNLATTAFI	209 QY 1014 KKGIDGED 209 Db 2147 KLSDDSVTVGTTDRILHGLDLNGG	269 QY 1052 KAEITAKDGRDLTI 269 I : 1   : :     : :     : :     : :     : :       : :       : :         : :	224 OY 1092 ADGHNVTENSKVKTSSSNGGR 324 Db 2267 QGGYTVANATHNYGMTSNGGSGLYV	362 QY 1133 KDITSLKTVNITASE
1022AHATASGKVRGTDAEALGGLIGRNLNAAINNASAHGDVSLQAGRYLGGLIGHN	QY 1178 -SGNTVSVSATVDLTTKSGSKIEAKSGEANVTSATGTIGGT   1   1   1   1   1   1   1   1   1	3 ISGNTVNVTANAGDLTVGNGAEINATEGAATLTAT	OY 1253 -GNTLTTEAGSSITSTKGQVDLLAQNGSIAGSINAANVT-LNTTGTLTTVAG :	QY 1303 SDIKATSGTLVINAKDAKLNGDASGDSTEVNAVNASGS	Qy 1341GSVTAATSSSVNITGDLNTVNGLNIISKDG 1370             :   :         Db 1304 GSLEGWQALILGASAGGDVTAGYDSYIGGLVGFSTATISGASASGRVG 1351	RESULT 6	Proventies protrainsporter protein yapH (imported) - Yersinia pestis (strain CO92) (5.5pecies: Yersinia pestis (C.5pecies: Yersinia pestis (Yersinia pestis (Yersi	Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G. and Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davies,	t, m., municalorid, m.; Simmonds, M.; Skelton, J.; Stevens, K.; Whiteher turne 413, 523-527, 2001 'Title: Genome sequence of Yersinia pestis, the causative agent of plan	Reference number: AB0001; MUID:21470413; PMID:11586360 -Accession: AD0123 -Status: preliminary -AD0123 - AD0123	A; Residues: 1-3705 < CKUR> A; Cross-references: GB:AL590842; PIDN:CAC89847.1; PID:g15979073; GSPDB:GN0017 C; Genetics: AppH	Query Match 8.1%; Score 602; DB 2; Length 3705; Best Local Similarity 21.7%; Pred No. 1.4e-16; Matches 413; Conservative 260; Mismatches 695; Indels 534; Gaps	RGCDHSTEKGSEKPARMKVRHLALKPLSAMLLSLGVTSIPQSVLA   :                 :   :   :   :   :	QY 69 SGLGGMDVVHGTA-TMQVDGNKTIIRNSVDAIINWKQFNIDQNEMYQFLQENNNSAVFNR 1		1138 NYREGITTVTAGELLIANGSGELLIANGS  1		GGVISAQNQQAKGG   :  NGANAAMTN	

JIIGGADTALTANNSGFL---GQYALAGNSKLTVASTN 1409 HEVTPPNVSLLEQDRGDILLELINAANVTGN----A 1636 ANINGYRQTVGAVTNSGAVTLGNGGVLTSGLLTNGGI 1816 GTFGNSVTGSGVLQVTDDAEVTLTSSNGVSNAVTIDI 1469 NVAKNDASTAFDFGSTVGGAFSGIVN-----LTNTT 1523 VTTVGATDR-TLHGLDLNGGTLIFDGSPPQSQANGVV 1581 :| | | : QQGGSTVANAIHNYGLTSSNGNGGSGLYVNYTLSALE 1696 NAELFGVGGLVVDAQNGALTLANGNNRYEGTTTVTAG 1756 GAGTLNINGGDLAVSATNSGLSGQTHIADVASVTLTG 1876 TOWNESTLISHLIENGVSESIANVESGVAGSTVDIIGG 1986 : ||:| :: :|: Q---VTDDAEVTLTSSNGVGNTVKVDIADATLNLNDI 2086 | : : : : : : : EDFGSTVGGAFSGIVNLTNTTFALSADNAAALARATL 2146 VVSG------BKGGFAIVWGDIALI------DG 401 /ETSGHD-----LFIKDNAIVD-----AKEWLLDF 442 IQIG-----GNISQKEGNLTISSDKINITKQITI 1013 | | | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :| | | | | 323 ...--KVTTTAGSTINATNGKASITTKTGDISGTIS 1178 NTGIND ---- EFPTGTGEASDPKKNSELKTTLTNTT 487 SINIGSNSHLILHSKGQRGGVQIDG------ 536 H----KNITL----DQGFLNITAASVAFEGGNNKARDA 585 -----SSSDATSNANLTIKTKELKLTE-DLSISGFN 1051 LOLIDADNVTGNANDLELMINGTTISAGGGVQSTVQ 2266 ------ESNSD-----NDTGLTITAKNVEVN 1132 -EGKDFRANNV----SLNGTG------ 616 -SGTINISGNITINQTTRKNTSYWQTSHDSHWNVSAL 668 TI------GNSNDGNSGAEAKTVTFNNVKDSKIS 1091 GLTTQYRSSAGVNFNG------VNGNM 708 ---KLKPN-----ENMNTSKPLPIRFLANITATG 746 INISNGANFTLNSHVRGDDAFKINKDLTINATNSNFS 806 TYNISILGGNVTLGGQNSS----SSITGN-ITIEKA 856 SSLLVNGSLSLTGENADIKGNLTISESATFKGKTRDT 916 KLGNVTNDGDLNITT------HAKRNQRSI 962

Db 2324 AELSGVGGLVVDAONGALTLANGNNRYEGTTTVTAGELILGANGAFGQTSLLNIASGA-S 2382  Oy 1179 GRTVSVSATVDLTFKSGSKIEAKSGEANVTSATGTIGGTI 1218	RESULT 7  T31105  Typothetical protein 2 - Haemophilus ducreyi C;Species: Hemophilus ducreyi C;Species: Hemophilus ducreyi C;Species: Ja. Garenopiilus ducreyi C;Species: Ja. Garenopiilus ducreyi C;Species: Ja. Garenopiilus ducreyi J. Bacteriol. 180, 6013-6022, 1998 R;Mard, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J. J. Bacteriol. 180, 6013-6022, 1998 R;Mardenopiilus ducreyi secretes a filamentous hemagglutinin-like protein. A;Reference number: Z20984; MuID:99030326; PMID:9811662 A;Status: pre-liminary; translated from GB/EMBL/DDBJ A;Molecula type: DNA A;Residues: 1-4919 < WARR> A;Gross references: EMBL:AF057696; NID:93929021; PID:93929023; PIDN:AAC79761.1 C;Genetics: A;Gene: IspA2 Guery Match Guery M	Best Local Similarity

οy	225 SVNGGS	ISLLAGOKITISDIINPTITYSIAAPENEAVNLGDIFAKGGNINVRA 277
Dp	279 SIEGDSKPAN	DVNTRD
Oy	278 ATIRNOGKES	KSGNIVLSAKEGEAEIGGVI
Dp	313NPKKP	NPKKPITDNTRKDNIAISGESAGSMYGRNIKFIVT 347
Oy	338 GAVIDLSGK	LGGDERGEGKNGIQLAKKTSLEKGSTINVSG 38
qq	348	DKGAGVNHQGVIFAEDDINILTDDGNSRLNKVYADYVRVVG 388
Οy	384 KEKGGFAIVI	KEKGGFAIVWGDIALI-DGNINAQGSGDIAKTGGFVETSGHDLFIKDNAIVDAKEWLLDF 442
qq	389 K	DIELANNGQIHADQQLILNATGHVKLNDGSSVISNNNLGISALNLTL 436
οy	443 DNVSINAEDPLF-	NNTGINDEFPTGTGEASDPKKNSELKTTLTNTTI 48
qq	437 ENATVSANN	VINDIKLNNLSKVSARAADLQSGNLNLDKASVLAHKLTLNISNDVSL 49
δλ	489 SNYLK-NAW	SNYLK-NAWTMNITASRKLTVNSSINIGSNSHLILHSKQRGGGV 532
QQ	497 NNOSKLSAN	NLKIKKVRDLNLNNSELSANNLTLNTSNNITLKNKSKFTAGNMTLNVTNNV 556
οy	533 QIDGDITSKGGNLTIY	SGG
qq	557 TLNNDSELA	NYTKNYTLNDASKLSANKLDLN
οy	573 VAFEG	GNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTG 616
Dp	: I: 611 LTFKKVKNV	LTFKKVKNVTLNNDSELAANNLSLNASHNVTLNNKSKLSAQKADIKAVNLTLNDTTELTA 670
Qy	617 KGLNIISSV	SVNNLTHNLSGTI-NISGNITINQTTRKNTSYMQTSHDSHW-NV 665
qq		NSTIITUNGTIAGIFANITIEKLNNKEKALILAEQNLNFTVNGSHYENK 724
Qy	666 SALNLETGANFTFIK-	NFTFIKYISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKE 714
qq	725 GDIVSKDKA	GDDITLI
οy	715 GAKVNFKLK	GAKVNFKLKPNENMNTSKPLPIRFLANITATGGGSVFFDIYANHSGRGAELKMSEI 770
qq	784 GTFTN	-SGNLTTVKTLDVGDIQNFTNKGNLTVGEDLHIKSKTKITNDGKLISIKNL 838
δy	771 NISNGANFT	NISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFYDGYARN 821
Dp	839 NISSEADFI	NNGTLLGIEALKIATKGNFTNKEKAILASNSLLDISVAEGKKTFNNG 894
Qy	822 AINSTYNIS	AINSTYNISILGGNYTLGGQNSSSSITGNITIEKAANVTLEANNAPNQQNIRDRVIKLGS 881
QQ	895 TIESGKNEN	TIESGKNLNITNTGAFLNVDNATIRSFGVLNITSTGNVSNNGT 937
δλ	882 LLVNGSLSL	LLVNGSLSLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGTAEIN-ITQCVV 938
QQ	938 LISNERLNIT	TTSBANETNESNGTVMSNGLLNIIA 970
δλ	939 KLGNVTNDG	3DLNITTHAKRNQRSIIGG-DIINKKGSLNITDSNNDAEIQ 986
qq	971 KQGNITNKN	KQGNITNKNLIASRQQLNLTAVADNITNDSNISNKIAVLHSLGNISLNSKDQVYNLGEIY 1030
Qy	987 IGGNISOKE	IGGNISQKEGNLTISSDKINITKQITIKKGIDGEDSSSDATSNAN 1031
qq	z	KNDVKLMGDITTKTKEGQASYKLYQASNG
δλ	1032 LTIKTKELK	LTIKTKELKLTEDLSISGFNKABITAKDGRDLTIGNSNDGNSGAEAKTVTFNNVKDSKIS 1091
qα	1087 LNIKGKFAD	SEII 112
Qy	1092 ADGHNVTLN	SSNGGRESNSDNDTGLTITAKNVEVNKDITSLKTVNITASEKVTT 115
qq	1129 NRGTIN	-TINVKNKLSYDSDVSFENNMQSQKVDLYTKIFEAKSDIELTFKTNGTHPVYL 1183
Qγ	1152 TAGSTINAT	TAGSTINATNGKASITTKTGDISGTISGNTVSVSATVDLTT-KSGSKIEAKSGEANVTSA 1210

1184 NEYSNANBEKKTÄNSENEHTINGEN, SPECIAL (1811) — [INT.] [I	Db 457 GSWSNSHQTETLKASELTAGKDLGLDAQGSITAQGAKLHANENVLVNAKDNINL 510	OY 448 NAEDPLENNTGINDEFPTGTGEASDPKKNSELKTTLTNTTISNYLKNAWTMNITASRKLT 507   1   1   1   1   1   1   1   1   1	OY 508 VNSSINIGSNSHLILHSKGQRGGGVQIDGDITSKGGNLTIYSGGWVDVH 556  bb 559 LAADNNVNITGSQVKGNQGAFVKTTQGDVVIDNALSETISKIDERTGTAFNITKSSH 615	QY         557 KNITLDQGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTG 616           Db         616 KNETGNDVNVIG 647	OY 617 KGLNIISSVNNLTHNLSGTINI	QY 647 TTRKNTSYWQTSHDSHWNVSALNLETGANFTFIKYISSNS 686	OY 687 KGLTTQYRSSAGVNF-NGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFLA 740  DD 763 KKQTDNTDTTISGGFSYTGGVDKVGSKADFQYDKQHTQTEVTKNRGSQTEVAG 815	QY 741 NITATGGGSVFEDIYANH-SGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTIN 799 1:	QY 800 ATMSNFSLRQTKDDFYDGYARMAINSTYNISILGGNVTL 838  DD 871 LDYSGVT-KPVKKAIEDGVNTTKPGNNTDLTKKVTARDAIANLANLSNLETPNVGVEVGI 929	QY 839 GGQNSSSITGNITIEKAANVTLEANNAPNQONIRDRVIKLG-SLLVN 885 	OY 886GSLSLTGENADIKGNLTISESATFKGKTRDTLNITGNTTNNGT 928	QY 929 AEINITQGVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSLNITDSNNDAEI 985   1   1   1   1   1   1   1   1   1	Y 986 QIGGNISQKEGNLTISSDKINITKQITIKKGIDGEDSSSDATSNANLTIKT 1036 :  :	y 1037 KELKLTEDLSISGFNKAEITAKDGRDLTIGNSNDGNSGAEAKTVTFNNVKDSKISAD 1093	y 1094 GHNVTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKDITSL 1138	y 1139	y 1171 GDISCTISGNTVSVSATVDLTTKSGSKIEAKSGEANVTSATGTIGGTIS 1219 :	y 1220GNTVNVTANAGDLTVGNGAEINATEGAATLTATGN 1254 :	y 1255 tltteagssitstkgqvdllaqngsiagsinaanvtlnttgtlttvagsdikatsgtlvi 1314  ::
		<u> </u>	<u> </u>			<u>а</u> п	<b>о</b> п	ge	о <u>п</u>	<b>σ</b> α	da	da .	δ δ	λο —	δλ Oλ	λο da	QQ QQ	da da	λο —
1118 1124 1124 1135 1135 1135 1135 1135 1135 1135 113	:	TGTIGGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEAGSSITSTK	GQVDLLAQNGSIAGSINAANVTLNTTGTLTTVAGSDIKATSGTLVINAKDAKLN-GDASG :	DSTEVNAVNASGSGSVTAATSSSVNITGDLNTVNGLNIISKDGRNTVRLRGKE    ::     - ::::    DSTKASEKYKKVENVDHKENIDEHKLNIGKHEITVPGVSFENLNNKNMDHQPDKLGE		A precursor - Proteus mirabilis	#text_change	ilis calcium-independent 7716	425657 1. DIT	77; Gabs	ALKPLSAMLLSLGVTSIPQSVLASGLQGMDVVHGTATMQVDGN 88	KTIIRNSVDAIINWKOFNISAVFNRVT :	SNQISOLKGILDSNGQVFLINPNGITIGKDAIINTNGFTASTLDISNENIKARNFTF			NQGKLSADSVSKDKSGNIVLSAKEGEAFIGGVISAQNQAKGGK :: 1   1   1	LMITGDKVTLKTGAVIDLSGKEGGETYLGGDERGEGKNGIQLAKKTSLEKGSTINVSG	KEKGGFAIVWGDIALIDGNINAQGSGDIAKTG	GEVETSGHDLFIKDNAIVDAKEWLLDFDNVSI 4

QQ	1429 TIADKTGIS-DETKAKIDQGFGKVGNGIKNIVTGAEGHTANADIKVT 1474	Db 411GRASAADLTLNGRLNASCAKAGLELKAEGA 440
Oy Dp	1315 NAKDAKLNGDASGDSTEVNAVNASGSGSVTAATSSSVNITGDLNTVNGLNIISKDGRNTV 1374 ::	QY 512 INIGSNSHLILHSKGQRGGGVQIDGDITSKGGNLTIYSGGWVDVHKNITLDQG 564  :
Oy Dp		FINITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLN
Oy Db	1434 -ITVNTQ 1439     :  1565 NETVNTK 1571	Qy 621 IISSVNNLTHNLSGTINISGNITINQTTRKNTSYWQTSHDSHWNVSALNLETGANFTFIK 680 :
RESULT H83135 probab	RESULT 9 H83135 probable adhesin PA4082 [imported] - Pseudomonas aeruginosa (strain PA01)	OY 681 YISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFLA 740  Db 558GLFARSSGTLSNLKLNNLRVSDNTYGSGPSSLGALV 593
Spe; Dat; Acc;	, 1000 Hickey,	QY 741 NITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINA 800
Jman; Lo	adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V. Nature 406, 959-964, 2000 A;Title: Complete genome sequence of Pseudomonas aeruqinosa PA01, an opportunistic pathd	OY 801 THSHFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGGQNSSSSITGNITIEKA-ANV 859 1::
; Ref ; Acc ; Sta ; Mol		QY 860 TLEANNAPNQQNIRDRVIKLGSLLVNGSLSLTGENADIKGNLTISESATFKGKTRDT 916 : 1 : 1   1   1   1   1   1   1   1   1
Res Cro Exp		QY 917 LNITGNFTNNGTAEINITQGVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSL 974
A; Gene: Query Best	PA4082  Match 7.5%; Score 553.5; DB 2; Length 1018; Local Similarity 22.6%; Pred. No. 2.5e-15;	QY 975 NITDSNNDAEIQIGGNISQKEGNLTISSDKINITKQITIKKGIDGEDSSSDATSNANL 1032  :       :     :     :     :
Mat Qy	ative 181; Mismatches 453; Indels 399; GraduavavselargedhyrekGSEKPARMKVRHLALKPLSAMLLSL	<pre>Qy 1033 TIKTKELKLTEDLSISGFNKAELTAKDGRDLTIGNSNDGNSGAEAKTVTFNNVKDSKISA 1092</pre>
oy .	MUNICIALALASVLASGLOGMUVVSGGSKRKGAFAGGARAALASVLALL 43 GVTSI-PQSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDAII-NWKQFNIDQNEM 11    :	QY 1093 DGHNVTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKDITSLKTVNITASEKVTTT 1152 
Oy Oy	GATALAPAYALESGGTVVGGSANGEIHLSGGNSLSVNQKVDKLIANMDSFSVAAGER 10 VQFLQENNNSAVFNRVTSNQISQLKGILDSNGOVFLINPNGITIGKDAIINTNGFTASTL 17	QY 1153 AGSTINATNGKASITTKTGDISGTISGNTVSVSATVDLTTKSGSKIEAKSGEANVTSATG 1212
9	101 VIFNOPSSSSIALNRVIGTRASDIOGRIDANGOVFLVNPNGVLFGRGAQVNVGGLVASTL 160 173 DISNENIKARNFTFEQTRDKALAELVNH-GLITVGRDGSVNLIGGKVKNEGVISVN 227 1	OY 1213 TIGGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEAGS-SITSTKGOV 1271      ::
Oy Ob	GGSISLLAGOKITISDIINPTITYSIAAPENBAVNLGDIFAKGGNINVRAAT 27   1	Oy 1272 DLLAQNGSIAGS 1283 
Oy Dp	280IRNQGKLSADSVSKDKSGNIVL-SAKEGEAEIGGVISAQNQQAKGGKLMITGDKVT 334 : :   :      :         :	RESULT 10 B99789 hemagglutinin/hemolysin-related protein [imported] - Escherichia coli (strain O157:H7
Qy	335 LKTGAVIDLSGKEGGETYLGGDERGEGKNGIQLAKKTSLEKGSTINVSGKEKGGFAIV 392     ::       ::       ::	C:Species: Escherichia coli C;Bate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: B99789 R;Hayashl, T.; Makino, K.; Ohnishl, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, C
ογ γ		nagawa, coli 015
o y	TISNYLKNAWTMNITASRKLTVNSS 51	A;Accession: B99789 A;Status: preliminary

: : : : : : : : : : : : : : : : : :	INIGSNSHLILHSKGQRGGGVQIDGDITSKGGNLTIYSGGWDVHKNITLDQG 564  :	FINITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTGKGLN 620 	IISSVNNLTHNLSGTINISGNITINOTTRKNTSYWOTSHDSHWNVSALNLETGANFTFIK 680 :	YISSNSKGLTTQYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIRFLA 740	NITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINA 800 	TNSNFSLRQTKDDFYDGYARNAINSTYNISILGGNVTLGGQNSSSSITGNITIEKA-ANV 859  ::	TLEANNAPNQONIRDRVIKLGSLLVNGSLSLTGENADIKGNLTISESATFKGKTRDT 916 	LNITGNFTNNGTAEINITGGVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINKKGSL 974   :  :  :  :	NITDSNNDABIQIGGNISQKEGNLTISSDKINITKQITIKKGIDGEDSSSDATSNANL 1032	TIKTKELKLTEDLSISGFNKABITAKDGRDLTIGNSNDGNSGABAKTVTFNNVKDSKISA 1092  :	DGHNVTLNSKVKTSSSNGGRESNSDNDTGLTITAKNVEVNKDITSLKTVNITASEKVTT 1152 	AGSTINATNGKASITTKTGDISGTISGNTVSVSATVDLTTKSGSKIEAKSGEANVTSATG 1212   :::	TIGGTISGNTVNVTANAGDLTVGNGAEINATEGAATLTATGNTLTTEAGS-SITSTKGQV 1271   ::		
							TLEANNAPNQONIRDRVIKL :   : HVAAQSTERNS							2 DLLAQNGSIAGS 1283                 3 DFKPQSHYGQIYGA 986	0
411	512	565	621 533	681 558	741	801	960	917	975	1033 819	1093	1153	1213 934	1272	RESULT 10
qq	OY Db	Q7 Op	O <sub>Y</sub>	Qy Db	Qy Db	Qy Db	Qy	Qy Db	Qy Db	δ O	Qy	QY	Oy Db	Qy Db	RES

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A; Molecule type: DNA
A; Residues: 1-1268 <-HAY>
A; Residues: 1-1268 <-HAY>
A; Cross references: GB:BA000007; PIDN:BAB34705.1; PID:g13360742; GSPDB:GN00154
A; Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                   Query Match 7.2%; Score 531.5; DB 2; Length 1268; Best Local Similarity 22.3%; Pred. No. 2.7e-14; Matches 351; Conservative 209; Mismatches 513; Indels 499; Gaps
                                                                                                                                                                                                                                                                                                                                             46 ALKPLSAMLLSLGVTSIPQSVLASGL--QGMDVVHGTATMQVDGNKTIIRNSVDAIIN-W 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 KQFNIDQNEMV------QFLQENNN-----SAVFNRVTSNQISQLKGILDSN 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 DNLNVDKNGVVFNNSANESSTSLAGNIQGNSNLTSGSAKVILNEVTSKNPSTINGMMEVA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 G---QVFLINPNGITIGKDAIINTN--GFTASTLDISNENIKARNFTFEQTKDKALAEIV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 GDKADLIIANPNGITVNGGGSINTGKLTLTTGTPDIQD-------DKLAGYSV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   199 NHGLITVGKDGSVN-----LIGGKVKNEGVISVNGGSISLLAGQKITISDIINPTI 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 NGGITTLGKLDNASPTEILSRNVVVNGKVSADELNVVAGNNYVNAAGQ-----V 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 TGSVSATGSRNGYSVDVAKLGGMYANKISLVSTEKGVGVRNLGVIAGGVNGVSIDSKGNL 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 V-----AKGGKLMITGDKVTL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 LNSNAQIQSASTINLTINGTLDNTTGTVTSVGTISLNINKNTIVNTRAGNISTMGD-1YV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        340 NSGTIDNTNGKLAAAGMLAVDTNNATLINSGKGSSVGIE-AGLVALKTGTLNNSNGQIRG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 TYSIAAPEN-----EAVNLGDIFAKGGNI--NVRAATIRNQGKLS--ADSVSKDKSGNI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 KTGAVIDLSGKEGGETYLGGD-----ERGEGKN-GIQLAKKTSLEKGSTINVSGKEKG 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         399 GY-----VGLESAALN-NNNGDIQTTG------DIAIISNGNVD------430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       388 GFAIVWGDIALIDGNINAQGSGDIAKTGGFVETSGHDLFIKDNAIVDAKEWLLDFDNVSI 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      448 NAEDPLFNNTGINDEFPTGTGE----ASDPKKNSELKTTLTNTTISNYLKNAWTMNITAS 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 ------NNKGL---IRSSTGHIVIGAAGSVNNGSTKTADTGSSDS------LGIIA- 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            504 RKLTVNSSINIGSNSHLILHSKGQRGGGVQIDGDITSKGGNLTIYSGGWVDVHKNITLDQ 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             472 -----DIGVEIGAN--------NINNGGQ--IASNGNVSLSSYSTID- 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564 GFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTGKGLNIIS 623
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                                                                                                                                                                                                                                                                                                                                                                                                      13 ALTPIAILMM----LSFPVASQAAGLVIKNGTVYNANGVPVVDINKP---NGSGLSHNIW 65
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hypothetical protein 21542 [imported] - Escherichia coli (strain 0157:H7, substrain E C.Species Escherichia coli (5.5pecies Escherichia coli (5.5pecies E856) e E85649 (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pecies E8564) (5.5pec
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A;Experimental source: strain 0157:H7, substrain EDL933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            992 SQKEGNLTISSDKINITKQITIKKGIDGEDSSSDATSNANLTIKTKELKLTEDLSISGFN 1051
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                                                                                                                                                                                                              757 GNLYNRNTIAAEKGLDIAALNGIENWKDISAGGDLTMNTNRHVTNNSNSNMVGQNIVINA 816
                                                                                                                                                                                                                                                                                                                                                                                             873 ------IIDSKGNVGNNRGNLHALNGVLSVKGNNLN-NDNGEIRGYG 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            913 -------DVTL-------ALTGNYDSYKGSLTSETG-DVTLTANI
708 QNSSSGTMIDNNATGFIASDK--NLSLEVVNS-----LTNYGWISGKGDVDVTVNN 756
                                                                                                   895 ADIKGNLTIS-----ESATFKG--KTRD------TLNITGNFTNNGTAE-----INI 933
                                                                                                                                                                                                                                                                                                                        934 TQGVVKLGNVTNDGDLNITTHAK-RNQRSIIG-GDIINKKGSLNITDSNNDAEIQIGGNI 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   943 ----VDNAYGL-IAGENVSVDAKSTIYNNTALIAANKKLVINAGGNLENRDGNNFLRNNG 997
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Best Local Similarity 22.3%; Pred. No. 2.7e-14;
Matches 351; Conservative 209; Mismatches 513; Indels 499; Gaps
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A,Reference number: A85480; MUID:21074935; PMID:11206551
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<u>&gt;</u> 4	103	KQFNIDQNEMVQFLQENNNSAVFNRVTSNQISQLKGILDSN 143	
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ΟŸ	1170	KIEAKSGEANVTSATGTIGGTISG 1220
QQ	Db 1000 ALFGITDNVGGIVGKEGVTLSAQNVYNNNSSIIAENGPLNLLS-RGTLDNTRALLSSG	SIIAENGPLNLLS-RGTLDNTRALLSSG 1056
Qγ	1221	NATEGAATLTATGNTLTTEAGS 1262
qq	Db 1057 ADAIIRAAGTFYNNYATTYSAGNLDVYAASLNNASDGRLEDNTATGVIASDKNLDLSVDN	
οy	1263 SITSTKGQVDLLAQNGSI	AGSINAANVTLNTTGTLTTVAGSDIKA 1307
QQ	Db 1117 SVINYGWISGKGDVHFNVLKGTLYNRNAIAADNALTINALNGVENFK-	DIVAG
Οy	Qy 1308 TSGTLVINAKDAKLNGDASGDSTEVNAVN-ASGSGSVTAATSSSVNITGDLNTVNGLNII	GSGSVTAATSSSVNITGDLNTVNGLNII 1366
qq	1174	NRGNIVGDYSLGVKTTGNIYNYLNML 1227
Qy	1367 SKDGRNTVRLRGKEIEVKYIQP	SAKRVLEKVKDLSDEERETLAKLGVSAVR 1426
QQ	1228 SYGVAGV	SANKVTNSGKDAVLGGFYGL 1254
Qy	Qy 1427 EVEPNNTITVNT 1438	
qq	Db 1255 ALEANETDNTGT 1266	
RESI T31: fild C;S	emagglutinin 1 - Haemophilus emphilus ducreyi -1999 #sequence revision 22	ducreyi -Oct-1999 #text_change 22-Oct-1999
C X X	T31102; Lumbley, S.R.; Latimer, J.L.	Cope, L.D.; Hansen, E
- E.	nophilus ducreyi secretes a	filamentous hemagglutinin-like protein.
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A; W	ype: DNA 1-4152 <war></war>	
( V V V	rences: EMBL:AF057695; NID:g39 1	329017; PID:g3929018; PIDN:AAC79757.1
ÖMÄ	Similarity 20.1%; Pro	ore 523.5; DB 2; Length 4152; ed. 0.2 fe-13; 1ndele 711. Gang 83.
Oy.	2	H 44
qq	m	:  :  SSNSKIAEDQEEEPDSLACSLSPLSSSIH 62
οy	45	KPLSAMLLSLGVTSIPQSVLASGLQGMDVVHGTATMQVDGNKTII- 92
qq	Db 63 LGLHNHSPLKVFKGKSLSVVLLSLMPATPLLAQQNYAEALNGKVYVDSQHSSTRIY	FPLLAQQNYAEALNGKVYVDSQHSSTRIY 118
Oy	93RNSVDAII	-NWKQFNIDQNEMVQFLQENNNSAVFNRVTSNQ 132
QQ	119 EQKTNDNSKDGIVVVEIANPEVDGVSDNRF	KEFNIPNSAVFNNSRTES 166
δλ	Qy 133 ISQLKGILDSNGQ	VELINPNGITIGKDA 160 : ::
qq	167 TSQLVGKLH	NIQGALEVAGKKADLIIVNPNGITLNGVK 226
Qy	Qy 161 IINTNGFTASTLDISNENIKARNFTFEQTKDKALAEIVNHGLITVGKDGSVNLIGGKV	KDKALAEIVNHGLITVGKDGSVNLIGGKV 218

-NI 273  : YNL 311	AKG 323	TIN 380   KII 410	WLL 440     LAL 439	TIS 489  :: FLN 499	rry 548   	FRA 607 :- v 600	AVS 666   : AVT 657	KEG 715 NTT 703	(AN 757   1  GN 763	FYD 816 WGT 812	852 4NK 872	G 886   	3 921 4KL 992	INK 970        1	) 1018 HI 1112	1G 1066   	GRESN 1115 
YSIAAPENE-AVNLGDI-FAKGGNI ::     :        - -TVAKTENQKSVNPANITFAAGSLNYNL	-VLSAKEGEAEIGGVISAQNQQAKG  ::	GIQLAKKTSLEKGSTIN  :   :   -IELTEKGQLQANNKII	OLFIKDNAIVDAKEWLL      ::   ADNVNVKSENLAL	KTTLTNTTI 	QIDGDITSKGGNL :: ::  TLNGEASLVAEKL	ANAKIVAQGTVTITGEGKDF    :  :   : -NALILAHQNLNFTVNGSHY	KNTSYWOTSH-DSHWNVS   :           : NNFNITQGSEIILHGNVT	VNFNGVNGNMSFNLKEG :  : :   : : LNISNIESFINAGNLTTGKNLEVHSNTT	GGGSVFFDIY   :  SNGSLASNKSLDIY	TNSNFSLRQTKDDFYD :	AVEHSNNDINENA		TRDTLNITG    : : QAKIINRGTINVKN	RNQRSIIGGDIINK   : :  :  1 SNRRRRASNDGEGTNK	INITKQITIKKGI)   : :  : NNTEGENYLKTAL(	AKDGRDLTION     :   :   :   :   :   :   :   :   :	
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KNEGVISVNGGSISLLAGOKITISDIINPTITX  ::	NVRAATIRNQGKLSADSVSKDKSGNIVLSAKEGEAEIGGVISAQNQO 	GKLMITGDKVTLKTGAVIDLSGKE :               - -NIKMDGGNASLKELYAKKDIDILAKD	VSGKEKGGFAIVWGDIALIDGNINAQGSGDIAKTGGFVETSGHDLFIKDNAIVDAKEWLL :: LNSADNVNVKSENIAL LNSADNVNVKSENIAL	DEDNVSINAEDPLFNNTGINDEFPTGTGEASDPKKNSELKTTLTNTT 	NYLK-NAWTMNITASRKLTVNSSINIGSNSHLILHSKGQRGGCVQIDGDITSRGGNLTIY           :       :	SGGWVD-VHKNITLDQGFLNITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRA 	NNVSLNGTGKGLNIISSVNNLTHNLSGTINISGNITINQTTRKNTSYWQTSH-DSHWNV 	ALNLETGANFTFIKYISSNSKGLTTQYRSSAGVNFNGVNG- 	AKVNFKLKPNENMNTS	H-SGRGAELKMSBINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQTKDDFY  	GYARNAINSTYNISILGGNVYLGGQNSSSSITGNIT	NIGE	SLSLTGENADTKGNLTISESATFKGKTRDTLNITG  :   :	FTNNGTAEINITQGVVKLGNVTNDGDLNITTHAKRNQRSIIGGDIINK 	KGSLNITDSNNDAEIQIGGNISQKEGNLTISSDKINITKQITIKKGID 	-GEDSSSDATSNANLTIKTKELKLT-EDLSISGFNKAEITAKDGRDLTIG 	NSNDGNSGAEAKTVTFNNVKDSKISADGHNVTLNSKVKTSSSNG
219 KN : 259 -D	274 NV 312 KT	324 GK 369 -N	381 VSG::: 411 LNS	441 DF : 440 EN	490 NY   500 NQ	549 SG : 554 A-	608 NN       601 NK	667 AL	716 AK       704 VK	758 H-	817 GY, 813 VM	853 873 VYI	887 SL           	922 NF	971 KG   1053 KT	1019 -GI   1113 FGI	1067 NS
Qy	Qy Db	Qy Db	Qy Dp	Q Dp	Oy Dp	Qy Dp	Q7 Dp	Oy Db	Oy Db	Qy Db	Qy Db	Qy Db	Qy Db	QY Dp	Qy	Qy Db	λα

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1173 VLRNGTNGVEDKVYQELNDKAKKEYEDKFAKKFQGRFKSRFQNGEFDWAGDWAKEGNESY 1232
                                                               1116 SDNDTGLTITAKNVEVNKDITSLKTVNITASE-KVTTTAGSTIN------- 1158
                                                                                                               1233 GSKET-----EEKYNGIKKEHTVNIGKHEIKVPTVSFENLNNINHQQDKSDGIDKSI 1284
                                                                                                                                                                                          1159 -----SITT 1168
                                                                                                                                                                                                                                                             1285 ISELLAQPIYVAKADVPDVDPRVAQNDKAVDEDGLYRTRLSYINQNNYLGAKYFFNQLDT 1344
                                                                                                                                                                                                                                                                                                                            1169 KTGDISG-----SATV---DLT 1191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : | : : | : : | : : | : : | 1.00 ADVINFMKRTRETETSLTHRNSEFNALSGELYVMGKADIGGVDI-NRDVEV-----IKT 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1192 TKSGS------ATGTI-- 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1215 ------GGTISGNTVNVTA----NAGDLTVGNGAEINATEGAATLTATGNTLT 1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1642 GDFNTKAGKDLFHRQIDTVTSGT--VYSASASGGGQSAGISLTDQGVETYTNKTATAGAN 1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1349 SSV-------NITGDLNTVNG-LNIISKDGRNTVRLRGKEIEVKYIQPGVAS 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1393 VEEVIEAKRVLEKVKDL---SDEERETLAKLGVSAVREVEPNNTITVNTQNEFTTRPSSQ 1449
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## RESULT 13 B81192

hemagglutinin/hemolysin-related protein NMB0497 [imported] - Neisseria meningitidis ( C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001

Circle 10. 181192

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Circle 10. 1. Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. I., H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoll, R.; A;Title: Complete genome sequence of Neiszesria meninglidas serogroup B strain MC58.

A; Accession: B81192

A;Status: preliminary A;Notecule type: DNA A;Rosidues: 1-1975 <TET> A;Ctross-references: GB:AE002406; GB:AE002098; NID:g7225720; PIDN:AAF40929.1; PID:g722 A;Experimental source: serogroup B, strain MCS8

A; Gene: NMB0497

Query Match 7.0%; Score 520; DB 2; Length 1975; Best Local Similarity 22.7%; Pred. No. 1.4e-13; Matches 384; Conservative 227; Mismatches 551; Indels 528; Gaps

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QQ	7	:: :       : :	09
δ δ	53	ATMOVDGNKTIIRNSVDA	98
an (	19	TOTPNGRGLSHN	7 .
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Qy	149		204
qq	171	TGAP	196
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٥y	243	SK	293
qq	254	!	307
٥y	294	DKSGNIVLSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYL :	L)
a a	308		339
δy	354	GGDERGEGKNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWG-DIALIDGNINAQGSGDIA	412
QQ	340		386
οy	413	NNTGIND-EFPTGT	467
qq	387		433
δy	468	GEASDPKKNSELKTTLTNTTISNYLKNAWTMNITASRKLTVNS	510
qq	434		493
Οý	511	SINIGSNSHLILHSKGQRGGGVQIDGDITSKGGNLTIYSGGWVDVHKNITLDQG	564
Dp	494		544
ΟY	565	FLNITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTGKGLNIISS	624
qq	545		585
οy	625	WQTSHDSHWNVSALNLETGANFTFIKY	681
QQ	586	AKGNIQL-RNTKLNAAKALETTA	620
Qγ	682	TOYRSSAGVNFNGVNGNMSFNLKEGAKVNFKLKPNENMNTSKPL	734
Dp	621	HVSLLA	629
QY	735	FTLNSHVRGDDAFKINK	794
Dp	099		683
٥y	795	DLTINATNSNFSLRQTKDDFYDGYARNAINSTY-NISILGGNVTLGCON-SSSSITGNIT	852
qq	684	DITLVAGNGIQLGDGKQRNSINGKHISIKNNGGNADLKNLNVHAKSGALNIH	735
δy	853	IEKAANVTLEANNAPNQQNIRDRVIKLGSLL	883
qq	736	SDRALSIENTKLESTHNTHLNAQHERVTLNQVDAYAHRHLSITGSQIWQNDKLF	795
٥ý	884	VNGSLSLTGENADIKGNLTISESATFKGKTRDTLNITGNFTNNGTA	941
qq	196	ANGVLALNARYSQIADNTTLRAGAINLTAG1	832
٥y	942	NVTNDGDLNITTHAKRNQRSIIGGDIINKKGSLNITDSNNDAEIQIGGNIS	992

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R:Perkhill, J: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Mature 413, 523-527, 2001
A.Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A.; Reference number: AB0001; MUID:21470413; PMID:11586360
A.Accession: AC0304
A.Scession: AC0304
A.Molecule type: DMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1051 NK-----AEITAKDGRDLTIGNSNDGNSGAEAKTVTFNNVKDSKISADGHNVTLNSKV 1103
                                                                                                                                                                                                                                                                                                                                                                                                   952 SNYFPTOKAAELNOK-SKELEQOIAQLKKSSPKSKLIP--TLQEERDRLAFYIQAINKEV 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1158 -----DISGTISG---- 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1180 ----NTVSVSATVDLTTKSGS------KIEAKSG-------EANV 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1126 KAPSGSIDIKAHSDIVLEAGQNDAYTFLKTKGKSGKIIRKTKFTSTRDHLIMPAPVELTA 1185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1208 TSATGTIGGTISGNTVNVTANAGDLTVGNGAEIN--ATEG----AATLTATGNTLTTEAG 1261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1262 SS-----ITSTKGQVDLLAQNGSIAGSINAANVTLNTTGTLTTVAGSDIKATSGTLVIN 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1316 AKDAKL-----NGDASGDSTEVNAV---NASGSGSV--TAATSSSVNITGDLNTVNGLN 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1365 I--ISKDGRNTVRLRGKEIEVKYIQPGVASVEEVIEAKRV----LEKVKDLSDEERETLA 1418
                                                                                                                               993 QKEGNLTISSDKINITKQITIKKGIDGEDS--SSDATSNANLTIKTKELKLTEDLSISGF 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1104 KTSSSNG-----GRESNSDNDTGLTITAKNVEVN-KDITSLKTVNITASEKVTTTAGSTI 1157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1066 AAILIDGITDQYEIGKPTYKSHYDKAALNKPSRLTGRTGVSIHAAAALDDARIIIGASEI 1125
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|: | :: | :: | :: | 833 NI-NWSTVSTKTLEDNAELKPLAGRINIEAGSGTLTIEPANRISAHTDLSIKTGGKLLLS 891
                                                                                                                                                                                                               892 AKGGNAGAPSAQVSSLEAKGNIRLVTGETDLRGSKITAGKNLVVATTKGKLNIEAVNNSF 951
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ος δ	9 (	IRNSVDAIINWKOFNIDONEMVOPLQENNNSAVENRVISNOISOLKGILDSNG-14
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oy B	145	-QVELINDOGIIGKDALININGFAST
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Ор	413	SGTLSVEASGKITAQGKNISGTAQRFTAHRLDLSGSQTQSRDITLIAQGGEIDLTGAE 470
δ	350	Ε-
Q D	471	LLASDRLSAATTALLRTDNASLIAEQITLDAQALSNVGGLIAHTGTTDFNLNLPGDVD 528
οy	382	EKGGFAIVWGDIALIDGNINAQGS 408
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λά	520	ASVA 57
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λά	575	FEGGITGEGKDFRANNVSLNGT 615
q	736	ATGALINHGEILTLGGLDTDSNTLFNTGSIISAEATLNARERITNSGPDALIGATDENGT 795
λ	616	GKGL-NIISSVNNLTHNLSGTINISG 640
q	196	LALLAPVIENSDTVTHTDTAPTTTILGMGTVILAGGHARDGHYASAAQVLNLSGLIESGK 855
λλ	641	NITINGTTRKN
ą	856	DMLIYATTLTNSRHILTANTDFIVADTVTGTAVWTAENPDIPGGRYAEPPDGGADNSDYI 915
λγ	099	NSKG
ą	916	GTEŸTSVIAYNGIDQISPEAQLLAGGNLTPQVGTLENFWSKVSAQGEIDLTGVTLQQDGW 975
ζ	693	YRSSAGV-NFNGVNGNMSFNLKE 714
ð	926	GDQORLMEQTTSSGVWRYRTYKGGLWTREWGPEVSERATSEYASSFTAKTLSGSGTTINN 1035
<u>^</u>	715 (	GAKVNFKLKPNENMNTSKPLPIRFLANITATGGGSVFFDIXAN 757
ā	1036	
٨	758	-HSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLTINATNSNFSLRQT 810

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1096	811	1150	870	677	7	1258	975	1307	1022	1355	1077	1407	1133	1467	1179	1527	1237	1580	1283	1630	1337	1680	1382	1721	1429	1776	
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A;Experimental source: serogroup B, strain MC58 C;Genetics: A;Gene: NMB1779

87; 61 SLVSLSMVLPAHAQITTDKSAPKNQQVVILKTNTGAPLVN----IQTPNGRGLSHN---- 112 :||||: | | |: :| 197 QIGKDGA--LTGFDVR-QGTLTVGAAGWNDKGGADYTGVLARAVALQGKLQGKNLAVSTG 253 297 GNIVLSAKEGEAEIGGVISAQNQQAKGGKLMITGDKVTLKTGAVIDLSGKEGGETYLGGD 356 471 SDPKKNSEL-----TVNSSIN 513 548 LSAASIHLKSDN-----AAH-----ITGTSKTLTASK-DMGVEAGSLNVTNT--N 589 627 NIVSDGL-----HAVSADGHVSLLANGNADFT------GHNTLTAKA---- 662 663 ------DVNAGSVGKG-RLKADNTNITSSSG-------DIT 689 798 INATNSNFSLRQTKDDFYDGYARNAINSTY-NISILGGNVTLGGQN-SSSSITGNITIEK 855 856 A---ANVTLEA--NNAPNQONIR-----------DRVIKLGSLLVNG 886 99 IINWKQFNIDQNEMYQFLQENNNSAVFN----RVTSNQI-----SQLKGILDSNGQ---VFL 148 149 INPNGITIGKDAIINTNGFTASTLDISNENIKARNFTFEQTKDKALAEIVNHGLIT---- 204 205 -VGKDGSVNLIGGKVKNEGVISV-----NGG-----SISL---LAGQKITIS-- 242 243 ----DIINPTITYSIAAPENEAVNLGDIFAKGGNINVRAATIRNQGKLSADSVS--KDKS 296 254 POKVDYASGEISAGTAAGTKPTIAL-DTAALGG--------MYADSITLIANEK 298 299 GVGVKNAGTLEAAKQLIVTSSGRIENSGRIATTAD-------GTEASPTYLSIE 345 357 ERGEGKNGIQLAKKTSLEKGSTINVSGKEKGGFAIVWG-DIALIDGNINAQGSGDIAKTG 415 416 GFVETSGHDLFIKDNAIVDAKEWLLDFDNVSINAEDPLF----NNTGIND-EFPTGTGEA 470 393 TTVLNAGHNLVIESKTNVN-------NAKGPATLSADGRTVIKEASIQTGTTVY 439 440 SSSKGNAELGNNTRITGADVTVLSNGTISSSAVIDAKDTAHIEAGKPLSLEASTVTSDIR 499 514 IGSNSHLILHSKGQRGGGVQIDGDITSK-----GGNLTIYSGGWVDVHKNITLDQGFLN 567 568 ITAASVAFEGGNNKARDAANAKIVAQGTVTITGEGKDFRANNVSLNGTGKGLNIISSVNN 627 628 LTHNLSGTINI---SGNITINQTTRKNTSYWQTSHDSHWNVSALNLETGANFTFIKYISS 684 N--SKGLTTQYRSSAGVNFNG-----VNGNMSFNLKEGAKVNFKLKPNENMNTSKPLPIR 737 738 FLANITATGGGSVFFDIYANHSGRGAELKMSEINISNGANFTLNSHVRGDDAFKINKDLT 797 Ouery Match 7.0%; Score 517.5; DB 2; Length 1995; Best Local Similarity 22.8%; Pred. No. 1.8e-13; Matches 385; Conservative 228; Mismatches 555; Indels 519; Gaps 53 MLLSLGVT-----SIP---QSVLASGLQGMDVVHGTATMQVDGNKTIIRNSVDA 98 1 MNK-IYRLKFSKRLNALVAVSELARGCDHSTEKGSEKPARMKVR-----HLALKPLSA 52 οχ ŏ qq Q qq ογ q δ Dp g g οy QQ δ ò qq ŏ ö ò

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